

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US 09/907,942
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-942-137

Query Match 98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7.8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEAKACRRDGGQVLSIES 52
DB 24 GRLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRLNFEAKACRRDGGQVLSIES 83
QY 53 EDEQKLIETIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNYYVDEP 112
DB 84 EDEQKLIETIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNYYVDEP 143
QY 113 SCGSEVCVMVHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDKEKPAVPSRAEGEET 172
DB 144 SCGSEVCVMVHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDKEKPAVPSRAEGEET 203
QY 173 ELTTPVLPETQEDAKTKFKESREAAALNLAY 204
DB 204 ELTTPVLPETQEDAKTKFKESREAAALNLAY 235
RESULT 20
US-09-907-942-137
Sequence 137, Application US/09907942
Publication No. US20030027146A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter

Query Match 98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7.8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEAKACRRDGGQVLSIES 52
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QY 53 EDEQKLIETIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNYYVDEP 112
DB 84 EDEQKLIETIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNYYVDEP 143

QY 113 SCSEVGVVYHQPAPAGIGGYPMFQWDDRCNNKNNFICKYSDEKPAVPSREAEGET 172
 Db 144 SCSEVGVVYHQPAPAGIGGYPMFQWDDRCNNKNNFICKYSDEKPAVPSREAEGET 203
 QY 173 ELTPVLPETQEDAKTKFKSREAAALNLAY 204
 Db 204 ELTPVLPETQEDAKTKFKSREAAALNLAY 235

RESULT 21

US-09-904-859-137
 ; Sequence 137, Application US/09904859
 ; Publication No. US20030036060A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/904,859
 ; CURRENT FILING DATE: 2001-07-12
 ; PRIOR APPLICATION NUMBER: 09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1998-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
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 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 137
 ; LENGTH: 382
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-09-904-859-137
 Query Match 98.7%; Score 1092; DB 10; Length 382;
 Best Local Similarity 96.2%; Pred. No. 7.8e-102; Indels 8; Gaps 1;
 Matches 204; Conservative 0; Mismatches 0;
 QY 1 GRLLS-----GQPVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI 52
 Db 24 GRLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI 83
 QY 53 EDEQKLEKFIENLIPSDGDFWIGLRRREKQSNSTACODLYAWTDGSIQFRNMYVDEP 112
 Db 84 EDEQKLEKFIENLIPSDGDFWIGLRRREKQSNSTACODLYAWTDGSIQFRNMYVDEP 143
 QY 113 SCSEVGVVYHQPAPAGIGGYPMFQWDDRCNNKNNFICKYSDEKPAVPSREAEGET 172
 Db 144 SCSEVGVVYHQPAPAGIGGYPMFQWDDRCNNKNNFICKYSDEKPAVPSREAEGET 203
 QY 173 ELTPVLPETQEDAKTKFKSREAAALNLAY 204
 Db 204 ELTPVLPETQEDAKTKFKSREAAALNLAY 235

RESULT 22

US-09-909-204-137
 ; Sequence 137, Application US/09909204
 ; Publication No. US20030036061A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/909,204
 ; CURRENT FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048

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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-204-137

Query Match
Best Local Similarity 98.7%; Score 1092; DB 10; Length 382;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLS-----GQVCRGCTGTCPCYKVIYFHDTSRLNFEAKACRRDGGQGVLSIES 52
Db 24 GRLSASDLRLRGQGPVCRGCTGTCPCYKVIYFHDTSRLNFEAKACRRDGGQGVLSIES 83
QY 53 EDEQKLEKFIENLLPSDGFWIGLRRREKQKSNSTACQDLYAWTDGSIQFRNYYVDEP 112
Db 84 EDEQKLEKFIENLLPSDGFWIGLRRREKQKSNSTACQDLYAWTDGSIQFRNYYVDEP 143
QY 113 SCGSEVCVMVHQPAPAGIGGYPYMFQWDDRCNNKNNFICKYDEKFAVPSREAEGEET 172
Db 144 SCGSEVCVMVHQPAPAGIGGYPYMFQWDDRCNNKNNFICKYDEKFAVPSREAEGEET 203
QY 173 ELTTPVLPETQEDAKTKFKESRAAALNLAY 204
Db 204 ELTTPVLPETQEDAKTKFKESRAAALNLAY 235

RESULT 23
US-09-904-820-137
; Sequence 137, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-820-137

Query Match
Best Local Similarity 98.7%; Score 1092; DB 10; Length 382;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLS-----GQVCRGCTGTCPCYKVIYFHDTSRLNFEAKACRRDGGQGVLSIES 52
Db 24 GRLSASDLRLRGQGPVCRGCTGTCPCYKVIYFHDTSRLNFEAKACRRDGGQGVLSIES 83
QY 53 EDEQKLEKFIENLLPSDGFWIGLRRREKQKSNSTACQDLYAWTDGSIQFRNYYVDEP 112
Db 84 EDEQKLEKFIENLLPSDGFWIGLRRREKQKSNSTACQDLYAWTDGSIQFRNYYVDEP 143
QY 113 SCGSEVCVMVHQPAPAGIGGYPYMFQWDDRCNNKNNFICKYDEKFAVPSREAEGEET 172
Db 144 SCGSEVCVMVHQPAPAGIGGYPYMFQWDDRCNNKNNFICKYDEKFAVPSREAEGEET 203
QY 173 ELTTPVLPETQEDAKTKFKESRAAALNLAY 204
Db 204 ELTTPVLPETQEDAKTKFKESRAAALNLAY 235
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Db 84 EDEQKLIKFENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNMYVDEP 143
QY 113 SCGSEVCVVMYHQPSAPAGIGGYPYFQWNNDRCKNNKNNFICKYSDKEKPAVPSREAEGEET 172
Db 144 SCGSEVCVVMYHQPSAPAGIGGYPYFQWNNDRCKNNKNNFICKYSDKEKPAVPSREAEGEET 203
QY 173 ELTTPVLPETQEDAKKTFKESREAALNLAY 204
Db 204 ELTTPVLPETQEDAKKTFKESREAALNLAY 235

RESULT 24
US-09-904-786-137
; Sequence 137, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,786
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-786-137

Query Match 98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7.8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GLLS-----GGPVCBGGTQPCYKVIYPHDTSRLNFEFEAKACRRDGGQGVSTES 52
Db 24 GLLSASDLRLGGQFVCGKGGTQPCYKVIYPHDTSRLNFEFEAKACRRDGGQGVSTES 83
QY 53 EDEQKLIKFENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNMYVDEP 112
Db 84 EDEQKLIKFENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNMYVDEP 143
QY 113 SCGSEVCVVMYHQPSAPAGIGGYPYFQWNNDRCKNNKNNFICKYSDKEKPAVPSREAEGEET 172
Db 144 SCGSEVCVVMYHQPSAPAGIGGYPYFQWNNDRCKNNKNNFICKYSDKEKPAVPSREAEGEET 203
QY 173 ELTTPVLPETQEDAKKTFKESREAALNLAY 204

Db 204 ELTTPVLPETQEDAKKTFKESREAALNLAY 235

RESULT 25
US-09-906-646-137
; Sequence 137, Application US/09906646
; Publication No. US20030039971A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,646
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-26
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; PRIOR FILING DATE: 1999-12-16
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 2000-01-05


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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-646-137
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Query Match      98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7,8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQVCRGCTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSI 52
Db 24 GRLISASDLRLGGQPCVCRGCTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSI 83
QY 53 EDEQKLEKFIENLLPSDGFWIGLRREEKQSNSTACODLYAWTDGSIQFRNYYVDEP 112
Db 84 EDEQKLEKFIENLLPSDGFWIGLRREEKQSNSTACODLYAWTDGSIQFRNYYVDEP 143
QY 113 SCGSEVCVVMYHQPSAPAGIGGPFYFQWDDRCNMKNFI CKYSDKPAVPSREAGEET 172
Db 144 SCGSEVCVVMYHQPSAPAGIGGPFYFQWDDRCNMKNFI CKYSDKPAVPSREAGEET 203
QY 173 ELTPVLPEETQEDAKKTFKESREAAALNLAY 204
Db 204 ELTPVLPEETQEDAKKTFKESREAAALNLAY 235
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Job time : 91.7224 secs

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OM protein - protein search, using sw model
Run on: September 9, 2004, 22:48:35 : Search time 25.0614 Seconds
(without alignments)
782.999 Million cell updates/sec

Title: US-09-887-855-2_COPY_24_227
Perfect score: 1106
Sequence: 1 GRLLSGQPVCRGGTQPCYK.....EEDAKKTFKESREAAALNLAY 204
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	182	16.5	1456	1 A36563	mannose receptor p
2	178.5	16.1	1455	1 A48925	mannose receptor p
3	177	16.0	1268	2 S52781	neurocan - mouse
4	174.5	15.8	1643	2 T14274	versican precursor
5	174.5	15.8	3381	2 T42389	versican precursor
6	174	15.7	1257	2 S28764	neurocan precursor
7	174	15.7	2397	1 A55335	versican precursor
8	174	15.7	2409	1 A60979	versican precursor
9	171	15.5	3562	2 A47171	chondroitin sulfat
10	170.5	15.4	1479	2 T42710	mannose receptor,
11	158.5	14.3	1340	2 A39808	proteoglycan core
12	158.5	14.3	2327	2 T42630	aggreacan - bovine
13	158.5	14.3	2415	1 A39086	aggreacan precursor
14	154.5	14.0	612	2 B42755	E-selectin precurs
15	153.5	13.9	2124	2 A28452	proteoglycan core
16	152	13.7	912	2 A54423	brevican precursor
17	149.5	13.5	459	2 T24425	hypothetical prote
18	149	13.5	321	1 LN4UER	IgE Fc receptor II
19	148.5	13.4	330	2 T46256	brevican - human (
20	148	13.4	253	2 E93130	protein F52E1.2 [1
21	147.5	13.3	2132	1 A55182	aggreacan precursor
22	147	13.3	883	2 S57653	brevican precursor
23	146.5	13.2	162	1 LNRC1	lectin BRA3-1 prec
24	146	13.2	2109	1 I50421	aggreacan precursor
25	145.5	13.2	742	2 Jc7595	scavenger receptor
26	145	13.1	883	2 S49126	brevican precursor
27	144.5	13.1	173	2 S10548	lectin - barnacle
28	144.5	13.1	372	2 S23936	L-selectin precurs
29	144.5	13.1	404	2 A46274	Hiv gp120-binding

30 143.5 13.0 129 2 JC4329 coagulation factor
31 143.5 13.0 372 1 A32375 L-selectin precurs
32 143.5 13.0 463 2 T26655 hypothetical prote
33 142.5 12.9 131 2 JC5058 bitiscetin alpha c
34 142 12.8 1487 2 S48719 phospholipase-A(2)
35 141.5 12.8 331 1 LNMSER Ige Fc receptor, 1
36 140.5 12.7 162 1 LNRC3 lectin BRA3-2 prec
37 140 12.7 370 2 S22124 L-selectin precurs
38 139 12.6 248 1 LN4UPS pulmonary surfacta
39 139 12.6 248 1 LN4UPS pulmonary surfacta
40 139 12.6 248 1 LN4UPS pulmonary surfacta
41 139 12.6 283 1 LN4HLS lectin precursor -
42 138.5 12.5 152 2 JC4690 coagulation factor
43 138.5 12.5 202 2 JC4031 tetranectin precur
44 138 12.5 280 2 T29200 hypothetical prote
45 137.5 12.4 309 1 S34198 Ige Fc receptor II

ALIGNMENTS

RESULT 1

A36563
mannose receptor precursor - human
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C/Accession: A36563; A60926; A44255; B44255; C44255; D44255; E44255; F44255; G44255; H44
R/Taylor, M.E.; Conary, J.T.; Lennartz, M.R.; Stahl, P.D.; Drickamer, K.
J. Biol. Chem. 265, 12156-12162, 1990
A/Title: Primary structure of the mannose receptor contains multiple motifs resembling c
A/Reference number: A36563; MUID:90324192; PMID:2373685
A/Accession: A36563
A/Molecule type: mRNA
A/Residues: 1-1456 <TAY>
A/Cross-references: GB:J05550; NID:G188675; PIDN:AAA59868.1; PID:G188676
A/Note: parts of this sequence, including the amino end of the mature protein, were conf
R/Seckwitz, R.A.B.; Sastre, K.; Bailly, P.; Warner, A.
J. Exp. Med. 172, 1785-1794, 1990
A/Title: Molecular characterization of the human macrophage mannose receptor: demonstrat
A/Reference number: A60926; MUID:91079783; PMID:2258707
A/Accession: A60926
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1333, T', 1335-1456 <EB>
A/Cross-references: GB:X55635
A/Note: translation of the nucleotide sequence is incomplete
A/Note: in the authors' translation additional residues Pro-Glu-Ile are shown after 497-
R/Kim, S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.
Genomics 14, 721-727, 1992
A/Title: Organization of the gene encoding the human macrophage mannose receptor (MRC1).
A/Reference number: A44255; MUID:93052405; PMID:1294118
A/Accession: A44255
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A/Molecule type: DNA
A/Residues: 155-233 'KGAL', 238-283; 346-428; 492-569; 631-714; 716-719; 783-820, 'N', 822-865; '
A/Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:118428,
C/Genetics:
A/Gene: GDB:MRC1
A/Cross-references: GDB:133759; OMIM:153618
A/Map position: 10p13-10p13
C/Suprafamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C/Keywords: duplication; lectin; tandem repeat; transmembrane protein
F/1-18/Domain: signal sequence #status predicted <SIG>
F/168-209/Domain: fibronectin type II repeat homology <2F1>
F/223-340/Domain: C-type lectin homology <LCH1>
F/362-486/Domain: C-type lectin homology <LCH2>
F/945-1079/Domain: C-type lectin homology <LCH3>

Query Match 16.5%; Score 182; DB 1; Length 1456;
Best Local Similarity 25.5%; Pred. No. 8.8e-08;
Matches 53; Conservative 37; Mismatches 61; Indels 54; Gaps 8;

Qy 19 YKVIYFHTSRRLNFBEAKCRDGGQLVSEDEQKLEKFIENLLPSDGFWIGLR 78

Db 807 YKDYQYFSKKEKTDNARAFCKRFGDLVSIQSESEKFLWKVY-NNNDQSAVFIGLL 865
QY 79 RREKQSNSTACQDLYAWTDSISQFRNYYVDEPCGS--EVCVVMHQPAPAGIGGPY 136
Db 866 ISLDKK-----FAWMDGSKVDYVSWATGEPNFANEDENCVTMY-----SNSGF----- 908
QY 137 MFQWDDRCNMKNFICKYSEK-----PAVPSREAGSEGTETLTTPVLPEETOE----- 185
Db 909 ---WINDINGYPNARICQHNSSINATVMP-----TWPSVPGCKEGWNYFSN 954
QY 186 -----EDAKTKFKESREAAAL 200
Db 955 KCFKIFGFMEERKQWQARKACI 978
RESULT 2
A48925
mannose receptor precursor, macrophage - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48925; S21320; PC2245
R:Harris, N.; Super, M.; Rits, M.; Chang, G.; Erezkowitz, R.A.
Blood 80, 2363-2373, 1992
A:Title: Characterization of the murine macrophage mannose receptor: demonstration that
A:Reference number: A48925; MUID:93043353; PMID:1421407
A:Accession: A48925
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1455 <HAR>
A:Experimental source: peritoneal macrophage
A:Note: sequence extracted from NCBI backbone (NCBIP:118733)
R:Harris, N.; Super, M.; Rits, M.; Chang, G.; Erezkowitz, R.B.
submitted to the EMBL Data Library, April 1992
A:Description: Characterization of the murine macrophage mannose receptor: Demonstration
on
A:Reference number: S21320
A:Accession: S21320
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-302, 'W', 303-1117, 'E', 1118-1455 <HA2>
A:Cross-references: EMBL:Z11974; NID:G52997; PIDN:CAA78028.1; PID:G52998
R:Harris, N.; Peters, L.L.; Eicher, E.M.; Rits, M.; Raspberry, D.; Eichbaum, Q.G.; Super
Biochem. Biophys. Res. Commun. 198, 682-692, 1994
A:Title: The exon-intron structure and chromosomal localization of the mouse macrophage
A:Reference number: PC2245; MUID:94128116; PMID:8297379
A:Accession: PC2245
A:Molecule type: mRNA
A:Residues: 35-105 <HA3>
C:Genetics:
A:Gene: Nrcl
A:Map position: 2
C:Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C:Keywords: membrane protein; receptor
C:KeyWords: fibronectin type II repeat homology <F9>
F:168-209/Domain: fibronectin type II repeat homology <LCH1>
F:361-485/Domain: C-type lectin homology <LCH1>
F:943-1077/Domain: C-type lectin homology <LCH2>
Query Match 16.1%; Score 178.5; DB 1; Length 1455;
Best Local Similarity 25.9%; Pred. No. 1.8e-07;
Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;
QY 19 YKVIYFHTSRLNFEAEKACRRDGGOLVSIQSESEKFLWKVY-NNNDQSAVFIGLL 78
Db 806 YKDYQYFSKKEKTDNARAFCKRFGDLVSIQSESEKFLWKVY-NNNDQSAVFIGLL 864
QY 79 RREKQSNSTACQDLYAWTDSISQFRNYYVDEPCGS--EVCVVMHQPAPAGIGGPY 136
Db 865 ISMDKK-----FIWMDGSKVDYVSWATGEPNFANEDENCVTMY-----TNSGF----- 907
QY 137 MFQWDDRCNMKNFICKYSEK-----YSDKFAVPSREAGSEGTETLTTPVLPEETOE----- 185

QY 186 -----EDAKTKFKESREAAALNL 202
Db 954 CFKIFGFANEKKSQMDAFQACKGL 978
RESULT 3
S52781
neurocan - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C:Accession: S52781
R:Rauch, U.; Forberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, February 1995
A:Description: Amino acid sequence of mouse neurocan and brevicin and their different ex
A:Reference number: S52781
A:Accession: S52781
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1268 <RAU>
A:Cross-references: EMBL:X84727; NID:G758629; PIDN:CAA59216.1; PID:G758630
C:Superfamily: agrican; C-type lectin homology; complement factor H repeat homology; EGI
F:176-253/Domain: link protein repeat homology <LNK1>
F:274-355/Domain: link protein repeat homology <LNK2>
F:964-995/Domain: EGF homology <EGF>
F:1040-1160/Domain: C-type lectin homology <LCH>
F:1167-1223/Domain: complement factor H repeat homology <FHD>
Query Match 16.0%; Score 177; DB 2; Length 1268;
Best Local Similarity 31.5%; Pred. No. 2.1e-07;
Matches 45; Conservative 17; Mismatches 49; Indels 32; Gaps 6;
QY 15 QRCYKVIYFHTSRLNFEAEKACRRDGGOLVSIQSESEKFLWKVY-NNNDQSAVFIGLL 74
Db 1048 QGHYR--YF---AHRRAWEDAEKRCRRAGHLTSVHSPEEHKFINSF-----GHENSW 1096
QY 75 IGLRREKQSNSTACQDLYAWTDSISQFRNYYVDEPS---CGSEVCVVMHQPAPAG 131
Db 1097 IGLNDRIVERD-----FQMTDNTGLQYENREKQPNFFAGGDCVVMVAHESG--- 1145
QY 132 IGGPYMFQWDDRCNMKNFICK 154
Db 1146 -----RWNDVPCNLYPVCK 1161
RESULT 4
T14274
versican precursor, splice form V2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C:Accession: T14274
R:Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 15758-15764, 1998
A:Title: Versican V2 is a major extracellular matrix component of the mature bovine brain
A:Reference number: Z17954; MUID:98288320; PMID:9624174
A:Accession: T14274
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1643 <SCH>
A:Cross-references: EMBL:AF060458; NID:G3253303; PID:G3253304; PIDN:AAC24360.1
A:Experimental source: brain
C:Keywords: glycoprotein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-1643/Product: versican, splice form V2 #status predicted <MAT>
F:57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent) #sta
Query Match 15.8%; Score 174.5; DB 2; Length 1643;
Best Local Similarity 25.8%; Pred. No. 4.7e-07;
Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;
QY 15 QRCYKVIYFHTSRLNFEAEKACRRDGGOLVSIQSESEKFLWKVY-NNNDQSAVFIGLL 73
Db 1424 QCCYK--YF---AHRPTWDAAPFCRIQAGHLTSILSHEEOMFVNRV-----GHDYQ 1471

```

F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1257/Product: neurocan #status predicted <MAT>
F;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;364-366/Region: cell attachment (R-G-D) motif
F;953-984/Domain: EGF homology <EGF>
F;1029-1149/Domain: C-type lectin homology <LCH>
F;1156-1212/Domain: complement factor H repeat homology <FHD>
F;121.339.737.967.1164/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;372.410/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F;944/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental

Query Match 15.7%; Score 174; DB 2; Length 1257;
Best Local Similarity 30.8%; Pred. No. 3.8e-07;
Matches 44; Conservative 18; Mismatches 49; Indels 32; Gaps 6;

QY 15 QRPCKVYIYFHTSRLNPFEEAKEACRRDGGOLVIESDEQKLEKTIENLLPSDGF 74
DB 1037 QGCHYR-YF--AHRRAWEADAERCRAGHLTSVHSPSEHKFINSF-----CHENS 1085
QY 75 IGLRREEKQSNSTACQDLAYWTDGSIQFRNRYVDEPS---CGSEVCVMVYHQSPAG 131
DB 1086 IGLNDRTVERD-----FQWDTGTQYENWREKQDPNFFAGGDCVMVAHENG--- 1134
QY 132 IGGPYMFQWDDRCNNKCNFICK 154
DB 1135 -----RWNDVPCNVNLPYVCK 1150

RESULT 7
A:55535
N:Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
vesican
N:Contains: glial hyaluronate-binding protein
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence,revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A:55535
R:ItO, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.
J. Biol. Chem. 270, 958-965, 1995
A:Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generate
A:Reference number: A:55535; MUID:95122551; PMID:7822336
A:Accession: A:55535
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2397 <RES>
A:Cross-references: GB:D16263; NID:9862460; PIDN:BA03796.1; PID:9862461
C:Superfamily: vesican; C-type lectin homology; complement factor H repeat homology; EG
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1654/Domain: vesican #status predicted <MAT>
F;167-244/Domain: link protein repeat homology <LNK1>
F;265-346/Domain: link protein repeat homology <LNK2>
F;2095-2126/Domain: link protein repeat homology <LNK1>
F;2133-2164/Domain: EGF homology <EG1>
F;2171-2291/Domain: C-type lectin homology <LCH>
F;2298-2354/Domain: complement factor H repeat homology <FHD>

Query Match 15.7%; Score 174; DB 1; Length 2397;
Best Local Similarity 28.5%; Pred. No. 8.1e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;

QY 15 QRPCKVYIYFHTSRLNPFEEAKEACRRDGGOLVIESDEQKLEKTIENLLPSDGF- 73
DB 2179 QGCHYR-YF--AHRRTWDAERCRAGHLTSILHSEEQFNVRV-----GHYDQ 2226
QY 74 WIGLRREEKQSNSTACQDLAYWTDGSIQFRNRYVDEP-----SCGSEVCVMVYHQSPAG 129
DB 2227 WIGL-----NDXMFEDHFRWTDGSLQYENWREKQDPNFFAGGDCVMVAHENG-- 2276
QY 130 AGIGGYPWFQWDDRCNNKCNFICKYS-----DEKPAVPSRAEGE 170
DB 2277 -----QWNDVPCNVNHLTYTCKKGTWACQGPVVENAKTFGK 2312

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RESULT 8
A60979
N:Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
N:Contains: glial hyaluronate-binding protein
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 19-Jan-2001
C:Accession: S06014; S43921; A60979; A30358; A29348; A45131; I54179
R:Zimmermann, D.R.; Ruoslahti, E.
EMBO J. 8, 2975-2981, 1989
A:Title: Multiple domains of the large fibroblast proteoglycan, versican.
A:Reference number: S06014; MUID:90059882; PMID:2583089
A:Accession: S06014
A:Molecule type: mRNA
A:Residues: 1-2409 <ZIM>
A:Cross-references: GB:X15998; NID:937662; PIDN:CAA34128.1; PID:937663
R:Yao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
A:Title: Identification of the proteoglycan versican in aorta and smooth muscle cells by
A:Reference number: S43921; MUID:95005762; PMID:7921538
A:Accession: S43921
A:Molecule type: mRNA
A:Residues: 208-440;1094-1385;1910-2246 <YAO>
R:Bignami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
Brain Res. 22, 67-70, 1989
A:Title: Structural similarity of hyaluronate binding proteins in brain and cartilage.
A:Reference number: A60979; MUID:89229983; PMID:2469524
A:Accession: A60979
A:Molecule type: protein
A:Residues: 171-210;289-303 <BIG>
R:Perides, G.; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
J. Biol. Chem. 264, 5981-5987, 1989
A:Title: Isolation and partial characterization of a glial hyaluronate-binding protein.
A:Reference number: A30358; MUID:89174663; PMID:2466833
A:Accession: A30358
A:Molecule type: protein
A:Residues: 24-50;80-87; 'D', 89-119;128-155;167-218;229-259, 'IR', 261-268;277-283, 'G', 285-
R:Krusius, T.; Gehlsen, K.R.; Ruoslahti, E.
J. Biol. Chem. 267, 13120-13125, 1992
A:Title: A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like
A:Reference number: A29348; MUID:88007514; PMID:2820964
A:Accession: A29348
A:Molecule type: mRNA
A:Residues: 1725, 'V', 1727-2409 <KRU>
A:Cross-references: GB:J02814
R:Perides, G.; Rahemtulla, F.; Lane, W.S.; Asher, R.A.; Bignami, A.
J. Biol. Chem. 267, 23883-23887, 1992
A:Title: Isolation of a large aggregating proteoglycan from human brain.
A:Reference number: A45131; MUID:93054750; PMID:1429726
A:Contents: brain
A:Accession: A45131
A:Molecule type: protein
A:Residues: 21-22, 'X', 24-37 <PE2>
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIP:118884)
R:Iozzo, R.V.; Naso, M.F.; Cannizzaro, L.A.; Wasmuth, J.J.; McPherson, J.D.
Genomics 14, 845-851, 1992
A:Title: Mapping of the versican proteoglycan gene (CSG2) to the long arm of human chr6
A:Reference number: I54179; MUID:93122792; PMID:1478664
A:Accession: I54179
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 251-347 <RES>
A:Cross-references: GB:I552488; NID:9263313; PIDN:AA824878.1; PID:9263314
C:Genetics:
A:Gene: GDB:CSG2
A:Cross-references: GDB:127873; OMIM:118661
A:Map position: 5q12-5q14
C:Superfamily: versican; C-type lectin homology; complement factor H repeat homology; EG
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-2409/Product: proteoglycan 24K core protein #status predicted <MAT>
F:167-244/Domain: link protein repeat homology <LNK1>

F:265-346/Domain: link protein repeat homology <LNK2>
F:559-1654/Domain: chondroitin sulfate attachment #status predicted <GAG>
F:2106-2137/Domain: EGF homology <EG1>
F:2144-2175/Domain: EGF homology <EG2>
F:2182-2302/Domain: C-type lectin homology <LCH>
F:2309-2365/Domain: complement factor H repeat homology <FHD>
Query Match 15.7%; Score 174; DB 1; Length 2409;
Best Local Similarity 28.5%; Pred. No. 8.1e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
QY 15 QPCYKVIYFHTSRLNFEBAKEACRRDGGQGLVSIIESEDEQKLEKFTENLLPSDGF- 73
Db 2190 QGQCYK--YF---AHRRTWDAARECRLOGAHLTSLSHSEEQFVNRI-----GHDIQ 2237
QY 74 WIGLRREEKQSNSTACQDLVATWDTGSIQFRNYYVDEP-----SCGSEVCVVMYHOPSAP 129
Db 2238 WIGL-----NDKMFEDFRWDTGSTLYQENWRPNQDPSFSSAGEDCVIIWHENG-- 2287
QY 130 AGTGGPYMFQWMDRRCNMKNFICKYS-----DEKPAVPSREAE 170
Db 2288 -----QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 2323
A:Reference number: A47171; MUID:93300846; PMID:8314802
A:Accession: A47171
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-3562 <SH1>
A:Cross-references: GB:D13542; NID:9391643; PIDN:BA02742.1; PID:9391644
A:Experimental source: stage 22-23 developing limb buds
A:Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
C:Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin
F:156-243/Domain: link protein repeat homology <LNK1>
F:254-345/Domain: link protein repeat homology <LNK2>
F:3258-3289/Domain: EGF homology <EGF1>
F:3296-3327/Domain: EGF homology <EGF>
F:3334-3454/Domain: C-type lectin homology <LCH>
F:3461-3517/Domain: complement factor H repeat homology <FHD>
Query Match 15.5%; Score 171; DB 2; Length 3562;
Best Local Similarity 28.5%; Pred. No. 2.4e-06;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
QY 15 QPCYKVIYFHTSRLNFEBAKEACRRDGGQGLVSIIESEDEQKLEKFTENLLPSDGF- 73
Db 3342 QGQCYK--YF---AHRRTWDAARECRLOGAHLTSLSHSEEQFVNRI-----GHDIQ 3389
QY 74 WIGLRREEKQSNSTACQDLVATWDTGSIQFRNYYVDEP-----SCGSEVCVVMYHOPSAP 129
Db 3390 WIGL-----NDKMFEDFRWDTGSTLYQENWRPNQDPSFSSAGEDCVIIWHENG-- 3439
QY 130 AGTGGPYMFQWMDRRCNMKNFICKYS-----DEKPAVPSREAE 170
Db 3440 -----QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 3475
RESULT 10
T42710
N:Alternate names: mannose receptor, macrophage - mouse
N:Alternate names: lambda lectin; phospholipase A2 receptor
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 09-Jun-2000

C:Accession: T42710
R:Wu, K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
A:Title: Characterization of a novel member of the macrophage mannose receptor type C le
A:Reference number: Z22235; MUID:9635501; PMID:8702911
A:Accession: T42710
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1479 <WUK>
A:Cross-references: EMBL:U56734; NID:gl336074; PID:AAAC52729.1
A:Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C:Keywords: membrane protein; receptor
F:186-227/Domain: fibronectin type II repeat homology <2FR>

Query Match 15.4%; Score 170.5; DB 2; Length 1479;
Best Local Similarity 31.4%; Pred. No. 9.4e-07;
Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;

Qy 5 SQPVCRGGTQPCVKYVYFHTDTSRLNFEAKACRRDGGQGVLSIESDEQKLEKFI 64
Db 384 SQPFF-----QHCYRL-----QAEKRWQSKRACLGGGDLLSHMALEPITKQIK 433
Qy 65 NLLPSDGGDFWGLRRREKQSNSTACQDLYAWTDSISQFRNYYVDEPS-----CGSEVCV 121
Db 434 QEVE---ELWIGL-----NDLKLQMNFEWSGSLVSFTWHHPFEPNFRDSDLCVT 482
Qy 122 MYHQSAPAGIGGPFYMFQWDDRCNMKNFICK 154
Db 483 IW----GPEG-----RWNDSPCNCQSLPSICK 504

RESULT 11
A39808
proteoglycan core protein, cartilage - bovine (fragments)
N:Alternate names: aggrecan; aggregating cartilage proteoglycan
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
A:Accession: A34234; A27752; A39808; A27751; E29164; B27751; D27751; F27
R:Antonsson, P.; Heinegard, D.; Oldberg, A.
J. Biol. Chem. 264, 16170-16173, 1989
A:Title: The keratan sulfate-enriched region of bovine cartilage proteoglycan consists o
A:Reference number: A34234; MUID:89390219; PMID:2528543
A:Accession: A34234
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 128-621 <ANT>
A:Cross-references: GB:J05028
R:Oldberg, A.; Antonsson, P.; Heinegard, D.
Biochem. J. 243, 255-259, 1987
A:Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a
A:Reference number: A27752; MUID:87270630; PMID:3111460
A:Accession: A27752
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 622-1340 <OLD>
R:Sandy, J.D.; Boynton, R.E.; Flannery, C.R.
J. Biol. Chem. 266, 8198-8205, 1991
A:Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation of
A:Reference number: A39808; MUID:91217051; PMID:2022637
A:Accession: A39808
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-28;59-82;131-137, 'QSET', 142-149;196-207;226-249;1137-1143;1252-1267;1274-1
R:Perin, J.P.; Bonnet, F.; Jolles, P.
FEBS Lett. 206, 73-77, 1986
A:Title: Structural relationship between link proteins and proteoglycan monomers.
A:Reference number: A27751; MUID:87005253; PMID:3530809
A:Accession: A27751
A:Molecule type: protein
A:Residues: 29-58;74-130;174-175, 'A', 177-204;208-225 <PER>
R:Perin, J.P.; Bonnet, F.; Jolles, P.
FEBS Lett. 176, 37-42, 1984
A:Title: Sequence data concerning the protein core of the cartilage proteoglycan monomer

A:Reference number: A91327; MUID:85027710; PMID:6489519
A:Accession: E29164
A:Molecule type: protein
A:Residues: 1230-1249 <PE2>
C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C:Keywords: glycoprotein
F:8-28/Domain: link protein repeat homology (fragment) <LNK1>
F:29-58/Domain: link protein repeat homology (fragment) <LNK2>
F:80-146/Domain: link protein repeat homology (fragments) <LNK3>
F:167-248/Domain: link protein repeat homology <LNK4>
F:1130-1250/Domain: C-type lectin homology <LCH>
F:1257-1313/Domain: complement factor H repeat homology <FHD>

Query Match 14.3%; Score 158.5; DB 2; Length 1340;
Best Local Similarity 26.8%; Pred. No. 9.7e-06;
Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;

Qy 7 QPVCRRG---TQPCYKVIYFHTDTSRLNFEAKACRRDGGQGVLSIESDEQKLEKFI 63
Db 1127 QKLCCEGWTKFQGHCYR--HFPD---RATWVDAESQCRKQKQSHLSIVTPEEQ----EFV 1177
Qy 64 ENLLPSDGGDF-WGLRRREKQSNSTACQDLYAWTDSISQFRNYYVDEP-----SCGSEV 118
Db 1178 NN---NAQDIQWIGL-----NDKTIEDFRWSGHSLOFENWRPNQDNFFATGEDC 1226
Qy 119 CVVMYHQSAPAGIGGPFYMFQWDDRCNMKNFICKYS-----DEKPAVPSREAEGETE 173
Db 1227 VVMWHEKG-----EWNDVPCNYQLPFTCKGTACGEPVVEHARIFGQKGD 1274

RESULT 12
T42630
aggrecan - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T42630
R:Hering, T.M.; Kollar, J.; Huynh, T.D.
submitted to the EMBL Data Library, September 1996
A:Description: Complete coding sequence of bovine aggrecan: comparative structural analy
A:Reference number: Z22182
A:Accession: T42630
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2327 <HER>
A:Cross-references: EMBL:U76615; NID:gl730259; PID:gl730260; PID:AA838524.1
A:Experimental source: articular chondrocytes
C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C:Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprot

Query Match 14.3%; Score 158.5; DB 2; Length 2327;
Best Local Similarity 26.8%; Pred. No. 1.8e-05;
Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;

Qy 7 QPVCRRG---TQPCYKVIYFHTDTSRLNFEAKACRRDGGQGVLSIESDEQKLEKFI 63
Db 2114 QKLCCEGWTKFQGHCYR--HFPD---RATWVDAESQCRKQKQSHLSIVTPEEQ----EFV 2164
Qy 64 ENLLPSDGGDF-WGLRRREKQSNSTACQDLYAWTDSISQFRNYYVDEP-----SCGSEV 118
Db 2165 NN---NAQDIQWIGL-----NDKTIEDFRWSGHSLOFENWRPNQDNFFATGEDC 2213
Qy 119 CVVMYHQSAPAGIGGPFYMFQWDDRCNMKNFICKYS-----DEKPAVPSREAEGETE 173
Db 2214 VVMWHEKG-----EWNDVPCNYQLPFTCKGTACGEPVVEHARIFGQKGD 2261

RESULT 13
A39086
aggrecan precursor, cartilage long splice form [invalidated] - human
N:Alternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; P
N:Contains: aggrecan cartilage short splice form
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000

A;Cross-references: GB:J05062; NID:g181167; PIDN:AAA35726.1; PID:g181168
C;Genetics:
A;Gene: GDB:AGC1; CSPGI; CSPGCP; MSX16
A;Cross-references: GDB:127479; OMIM:155760
A;Map position: 15q26-15q26
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF repeats; alternative splicing; cartilage; chondroitin sulfate proteoglycan; extracellular matrix
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2415/Product: aggrecan cartilage long splice form #status predicted <MATL>
F;20-2162,2201-2415/Product: aggrecan cartilage short splice form #status predicted <MATH>
F;20-2162,2201-2329,'A','2392-2415/Product: aggrecan short splice form #status predicted <MATI>
F;44-135/Domain: immunoglobulin homology <UMW>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;495-572/Domain: link protein repeat homology <LNK3>
F;593-673/Domain: link protein repeat homology <LNK4>
F;677-861/Domain: keratan sulfate attachment #status predicted <KSA>
F;864-1510/Domain: chondroitin sulfate attachment #status predicted <CS1>
F;1511-2152/Domain: chondroitin sulfate attachment #status predicted <CS2>
F;2168-2198/Domain: EGF homology <EGF>
F;2205-2325/Domain: C-type lectin homology <LCH>
F;2332-2388/Domain: complement factor H repeat homology <FHD>
F;426,239,333,387,434,602,657,737,1898/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;371,376/Binding site: keratan sulfate (Thr) (covalent) #status predicted

Query Match 14.3%; Score 158.5; DB 1; Length 2415;
Best Local Similarity 29.1%; Pred. No. 1.9e+05;
Matches 52; Conservative 22; Mismatches 62; Indels 43; Gaps 11;

QY 7 QPVCRGG---TORPCYKYIVFDHTSRRLNFBEAKEACRRDGGQLVSISEDEQKLIEKFI 63
Db 2202 QEVCCEGWNKYGHCYR--HPED---RETWDABRCREQSHLSIVTPEEQ----EFV 2252

QY 64 ENLLPSGDGP-WIGLRREESQSNTACQDLVANTDGISIFRWYVDSPS---CGSEVC 119
Db 2253 NN---NAOQYQWIGL-----NDRTTEGDFRSDGHPMQFNWRPNQPDPFFAAGEDC 2301

QY 120 VVM-VHOPSAPAGICPGYMFWNQDDRCNMKNFKCYKSY---DEKPVPFSREARGESTE 173
Db 2302 VMNIWHERG-----ENWDVPCNYHLFPFCCKGTACGEPPVVEHARTFGKKD 2349

RESULT 14
B42755
E-selectin precursor - mouse
N;Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1)
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000 #text_change 02-Aug-2002
C;Accession: S23174; B42755
R;Becker-Andre, M.; van Riel, J.; Losberger, C.; Whelan, J.; Delamater, J.F.
Eur. J. Biochem. 206, 401-411, 1992
A;Title: Murine endothelial leukocyte-adhesion molecule 1 is a close structural and functional homolog of human E-selectin.
A;Reference number: S23174; PMID:92283265; PMID:1375914
A;Accession: S23174
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-612 <BEC>
A;Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
R;Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A;Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-selectin mRNA in activated endothelial cells.
A;Reference number: A42755; PMID:92340571; PMID:1375846
A;Accession: B42755
A;Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A;Residues: 'MKATAGV', 1-389, 391-612 <WEL>
A;Cross-references: GB:M87862; NID:g193107
A;Experimental source: endothelial cells
A>Note: sequence extracted from NCBI backbone (NCBP:109470)
A>Note: the sequence in Genbank entry MU5ESELEC, release 117.0, (PIDN:AAA37577.1; PID:g193107), contains a premature stop codon at Met-1 or the AUG codon preceding that.
C;Superfamily: P-selectin; C-type lectin homology; complement factor H repeat homology; I-C;Keywords: glycoprotein; transmembrane protein

F;1-21/Domain: signal sequence #status predicted <SIG>
F;12-138/Domain: C-type lectin homology <LCH>
F;22-612/Product: P-selectin #status predicted <MAT>
F;143-174/Domain: EGF homology <EGF>
F;180-238/Domain: complement factor H repeat homology <FH1>
F;243-300/Domain: complement factor H repeat homology <FH2>
F;305-363/Domain: complement factor H repeat homology <FH3>
F;368-426/Domain: complement factor H repeat homology <FH4>
F;431-489/Domain: complement factor H repeat homology <FH5>
F;494-548/Domain: complement factor H repeat homology <FH6>
F;25,391,528/Binding site: carbonylrate (Asn) (covalent) #status predicted

Query Match 14.0%; Score 154.5; DB 2; Length 612;
Best Local Similarity 27.9%; Pred. No. 8.8e+06;
Matches 38; Conservative 28; Mismatches 45; Indels 25; Gaps 5;

QY 23 YFHTDTRRLNFEAKACRRDDGQLVSIKIEFKFIENLPDSGDGFWIGLRREE 82
:::
Db 23 YYNASSELMTYDEASAYCQRDYTHLVAIQNKEE---INVLNSLNKHSPSYVMIGIRK--- 76
:::
QY 83 KQSNSTACQDIYAWTDGS-----ISQFNWYVDERS--CGSEVCVVMYHQPSAPAGIGPYM 137
:::
Db 77 -----VNNVTWVGTKPLTEAQNWGPENNQRNECDCEIYIQTKOSGM----- 124
:::
QY 138 FQWNDRRCNMKNFIC 153
:::
Db 125 --WNDERCNKKLALC 138
::: :

RESULT 15
A28452
proteoglycan core protein precursor, cartilage - rat
N;Alternate names: aggrecan
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C;Accession: A92623; A28353; A28453; A28095; A28452
R;Doerge, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 262, 17757-17767, 1987
A;Title: Complete primary structure of the rat cartilage proteoglycan core protein deduced from complementary DNA sequence
A;Reference number: A92623; MUID:98087070; PMID:3693370
A;Accession: A92623
A;Molecule type: mRNA
A;Residues: 1-2124 <DOE>
R;Doerge, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 263, 10040a, 1988
A;Reference number: A30069
A;Contents: annotation; revision to residue 698
R;Doerge, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 261, 8108-8111, 1986
A;Title: Partial cDNA sequence encoding a globular domain at the C terminus of the rat cartilage proteoglycan aggregates. The link protein and proteoglycan amino-terminal domains are located in separate genes
A;Reference number: A28353; MUID:86250698; PMID:2424893
A;Accession: A28353
A;Molecule type: mRNA
A;Residues: 1856-2124 <DO2>
A;Cross-references: GB:M13518; NID:g206104; PIDN:AAA41836.1; PID:g206105
R;Neame, P.J.; Christner, J.E.; Baker, J.R.
J. Biol. Chem. 262, 17768-17778, 1987
A;Title: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-terminal domains are located in separate genes
A;Reference number: A28453; MUID:88087071; PMID:3693371
A;Accession: A28453
A;Molecule type: Protein
A;Residues: 20-37, W,39-60, 'E',62-64, 'X',66-69,70-83,84,89-148,'L',150-238,'S',240,'A','B',242-243,
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2124/Product: proteoglycan core protein #status predicted <MAT>
F;44-135/Domain: immunoglobulin homology <IMW>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;1914-2034/Domain: C-type lectin homology <LCH>
F;2041-2097/Domain: complement factor H repeat homology <FHD>

	Query Match	13.5%;	Score 149;	DB 1;	Length 321;
	Best Local Similarity	30.2%;	Pred. No. 1.3e-05;		
	Matches 55;	Conservative 20;	Mismatches -57;	Indels 50;	Gaps 11;
Qy	15	QRCKYVIYFHTSRLRNLFEEAKACRRDGGQLVSISEDEQKLEFIENLLPSDGDFW	74		
		: : : : :			
Db	171	QRCKCY---YFGKTKQ--WHARYACDDMEGQLYSIHSPEDFLTKH----	ASHTGSW 220		
		: : : : :			
Qy	75	IGLRRREBKQSNSTACQDLVAWTGSIQFNWYVDPSCGS--EVCVVWYHQPSAPAGI	132		
		: : : : :			
Db	221	IGLRNLDLKG-----FTWDGSHVDYNWAPEGFTSRSGEDCVWM-----	RGS 265		
		: : : : :			
Qy	133	GGPFNFOWNDRRCNMK--NNFTCKYSDEKPAV---PSRAEGE-----	EVELTTPV 178		
		: : : : :			
Db	266	G-----RWNDAFCDRKLGAWYC----DLRATCTPASEGSABSMGPDSPDPDKRLPTFS	316		
		: : : : :			
Qy	179	LP 180			
		: : : : :			
Db	317	AP 318			

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RESULT 19
T46256
Dreikan - human. (fragment)
N;Alternate names: protein DKFzp761l191.1
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
C;Accession: T46256
R;Ottewaelde, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23031
A;Accession: T46256
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-330 <AAA>
A;Cross-references: EMBL:AL137504
A;Experimental source: adult amygaala; clone DKFzp761l191
C;Genetics:
A;Note: DKFzp761l191.1

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Query Match	13.4%;	Score 148.5;	DB 2;	Length 330;
Best local Similarity	29.5%;	Pred. No. 1.5e-05;		
Matches	46;	Conservative 16;	Matches 57;	Indels 37; Gaps 8;
Qy	6	QGPVCRGG---TQPPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSIESDEOKLIEKF	62	
Db	103	GLRFENPGWDAFQAGCYK-----HFSTRK-SWEEAETQCRMYGAHLASISTPEEQDINNRR	157	
Qy	63	IENLLPSDGDWIGLRREEKQSNSTACQDLYAWTGDGISQFRNMYVDPS---CGSEVC	119	
Db	158	YREYQ-----WIGL-----NDRTEGDFLMSDGVPLIYENWNPQPSYFLSGENC	203	
Qy	120	VVM-YHQPSPAGIGGPYMFQWDDRCNMKNFNICK	154	
Db	204	VVMYWHDOG-----QWSIVPCNHYHLSYTC	228	

RESULT 20
E89130
protein F52E1.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: E89130
R:anonymous, The C. elegans Sequencing Consortium.
Science 284, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; PMID:9089613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: E89130
A>Status: preliminary

```

A:Molecule type: DNA
A:Residues: 1-253 <STO>
A:Cross-references: GS:chr_V; PIDN:AAE37037.1; PID:g1086809; GSPDB:GN00023; CESP:F52E1.2
C:Genetics:
A:Gene: F52E1.2
A:Map position: 5

Best Match
      13.4%   Score 148;   DB 2;   Length 253;
      Local Similarity 29.2%;   Pred. No. 1.2e-05;
      Matches 49;   Conservative 24;   Mismatches 57;   Indels 38;   Gaps 10;

Qy 10 CRGS-----TQPCVKV-IYFHDTSRRRLNPEE-----AKEACRRDGGOLVSIES 52
Db 96 CPGCGPTGQWYLNASKCYKVLHFLCHLSLKVLQKQFDAAVTYAGATSACAQAELVTIDS 155
Qy 53 EDEOKLIEKIEN---LLPSDGDGFWIGLRREEEQKSNACODLYANTDGSISOFRWYVD 110
Db 156 FDENDALRKAFDYNALVDETKFTWIGK-----SLSGAWQ-----WADGSSATITNWAPS 205
Qy 111 EPSCGSRVCCVMYHQSAPAGIGPYMFQ---WNDRCCNMKN-NFTCK 154
Db 206 QPS--SNGLCYQMITDLSNA-----TVKYQRGGWKTYCGCKTSASYICE 248

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RESULT 21

A55182

aggreacan precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jan-2000

C:Accession: A55182; S55329; S50207; S51355; I78532; I58123

E:Walcz, E.; Deak, F.; Erhardt, P.; Coulter, S.N.; Fueuloep, C.; Horvath, P.; Doege, K.J.

Genomics 22, 364-371, 1994

A:Title: Complete coding sequence, deduced primary structure, chromosomal localization, A:Reference number: A55182; MUID:95104847; PMID:7806222

A:Accession: A55182

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-2132 <WAL>

A:Cross-references: GB:I07049; NID:G578541; PID:RAC37670.1; PID:G191772

R:Watanabe, H.; Gao, L.; Sugiyama, S.; Doege, K.; Kimata, K.; Yamada, Y.

Biochem J. 308, 433-440, 1995

A:Title: Mouse aggreacan, a large cartilage proteoglycan: protein sequence, gene structure A:Reference number: S55329; MUID:95289972; PMID:7772024

A:Accession: S55329

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-567, 'G', 569-1728, 'I', 1730-2132 <WAT1>

A:Cross-references: GB:U22901; NID:G886014

R:Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.

Biochim. Biophys. Acta 1219, 613-622, 1994

A:Title: Analysis of aggreacan and tenascin gene expression in mouse skeletal tissues by A:Reference number: S50206; MUID:95035091; PMID:7524681

A:Accession: S50207

A:Molecule type: mRNA

A:Residues: 350-481, 'R', 483-506 <GLU1>

A:Cross-references: EMBL:X80279; NID:G673432

R:Glumoff, V.

submitted to the EMBL Data Library, July 1994

A:Reference number: S51355

A:Accession: S51355

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 350-383, 'CPVNSQRERPWAA' <GLU2>

A:Cross-references: EMBL:X80279

R:Watanabe, H.; Kimata, K.; Line, S.; Strong, D.; Gao, L.Y.; Kozak, C.A.; Yamada, Y.

Nature Genet. 7, 154-157, 1994

A:Title: Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in the aggreacan A:Reference number: I58123; MUID:95004579; PMID:7920633

A:Accession: I78532

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 211-326 <WAT2>

A:Cross-references: GB:S73722; NID:G765215; PID:RAB32160.1; PID:G765216

A:Accession: J59123
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 211-240, 'MCTASLRWRVSRVHFRQNSRRQTS', 'AGGWCHAMPQASSTWFGRAWVTCALAGW', 'R
A:Cross-references: GB:S73720; NID:G765211; PIDN:AA332159.1; PID:G765212
C:Genetics:
A:Map position: 7
A:Introns: 253/1
C:Superfamily: aggrecan, C-type lectin homology; complement factor H repeat homology; EG
C:Keywords: cartilage; extracellular matrix
F:1-13/Domain: signal sequence #status predicted <SIG>
F:14-135/Domain: immunoglobulin homology <IMM>
F:170-247/Domain: link protein repeat homology <LNK1>
F:268-349/Domain: link protein repeat homology <LNK2>
F:504-581/Domain: link protein repeat homology <LNK3>
F:502-683/Domain: link protein repeat homology <LNK4>
F:1922-2042/Domain: C-type lectin homology <LCH>
F:2049-2105/Domain: complement factor H repeat homology <FHD>
Query Match 13.3%; Score 147.5; DB 1; Length 2132;
Best Local Similarity 24.7%; Pred. No. 0.00016;
Matches 45; Conservative 30; Mismatches 64; Indels 43; Gaps 9;
QY 4 LSGQPVCRGG---TORPCVKVIYFHTDSRLNFEAKACRRDGGQGVLSIESEDEQKLE 60
DB 1916 VADQCEQCEGWTKFQGHCVYR--HFED---RETWVDAERRCRQQSHLSIVTPEEQEFVN 1970
QY 61 KFIENLLPSDGDGF-WIGLRREKQSNSTACQDLYAWTDGSIQSFRNMYVDEP---SCG 115
DB 1971 KNAQ-----DYQWIGL-----NRTIEGDFRWDGSHLSQPEKRWQPNDFPATG 2015
QY 116 SEVVCVVMYHQPAPAGIGGPFYFQWDDRCNNKNNFICKYS---DEKPAVPSREAECEE 171
DB 2016 EDCVVMWHERG-----ENNDVPCNQLPFTCKGTGACGDPVVEHARTLQOK 2064
QY 172 TE 173
DB 2065 KD 2066
RESULT 22
S57653
brevican precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
C:Accession: S57653
R:Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, May 1995
A:Description: Cloning and sequence of mouse neurocan and brevican and their different e
A:Reference number: S57653
A:Accession: S57653
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-883 <RAU>
A:Cross-references: EMBL:X87056; NID:G886889; PIDN:CAA60575.1; PID:G886890
C:Superfamily: aggrecan, C-type lectin homology; complement factor H repeat homology; EG
F:49-138/Domain: immunoglobulin homology <IMM>
F:173-250/Domain: link protein repeat homology <LNK1>
F:271-352/Domain: link protein repeat homology <LNK2>
F:626-657/Domain: EGF homology <EGF>
F:564-784/Domain: C-type lectin homology <LCH>
F:791-847/Domain: complement factor H repeat homology <FHD>
Query Match 13.3%; Score 147; DB 2; Length 883;
Best Local Similarity 29.7%; Pred. No. 6.2e-05;
Matches 43; Conservative 21; Mismatches 45; Indels 36; Gaps 8;
QY 15 QRPCVKVIYFHTDSRLNFEAKACRRDGGQGVLSIESEDEQKLI-EKFIENLLPSDGDGF 73
DB 672 QGACIK----HFSTR-SWEAEASQCRALGALHTSICTPEDQFVNDRYREYQ----- 719
QY 74 WTGLRRREKQSNSTACQDLYAWTDGSIQSFRNMYVDEPS---CGSEVVCVM-HQPSAP 129

DB 720 WIGL-----NDRTIEGDFLMSDCAPLLYENWNPQDPSYFLSGCNCVVMVWHDQG-- 769
QY 130 AGTGGPFYFQWDDRCNNKNNFICK 154
DB 770 -----QWSDVPCNYHLSTCK 785
RESULT 23
LNRC1
lectin BRA3-1 precursor - barnacle (Megabalanus rosa)
C:Species: Megabalanus rosa
C:Date: 24-Feb-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C:Accession: JCI503; A26094
R:Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T.
Gene 128, 251-255, 1993
A:Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure and
A:Reference number: JCI503; MUID:93292994; PMID:8514190
A:Accession: JCI503
A:Molecule type: DNA; mRNA
A:Residues: 1-162 <FAK>
A:Cross-references: DDBJ:D13299
R:Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-295, 1986
A:Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
A:Reference number: A26094
A:Accession: A26094
A:Molecule type: protein
A:Note: 146-Arg was also found
C:Comment: This galactose-binding lectin is isolated from the coelomic fluid.
C:Comment: This protein plays important roles in defense mechanisms and in development ar
C:Comment: The molecule is a tetramer of identical chains.
C:Genetics:
A:Introns: 22/1; 47/2; 86/3
C:Superfamily: tetranectin, C-type lectin homology
C:Keywords: hemolymph; homotetramer; lectin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-162/Product: lectin BRA3-1 #status experimental <MAT>
F:26-150/Domain: C-type lectin homology <LCH>
F:26-39,56-150,125-142/Disulfide bonds: #status experimental
F:157/Disulfide bonds: interchain (to 160) #status experimental
F:160/Disulfide bonds: interchain (to 157) #status experimental
Query Match 13.2%; Score 146.5; DB 1; Length 162;
Best Local Similarity 25.0%; Pred. No. 9.6e-06;
Matches 40; Conservative 26; Mismatches 59; Indels 35; Gaps 6;
QY 3 LLSQPVCRGGTORPCVKVIYFHTDSRLNFEAKACR--RDGGQGVLSIESEDEQKLE 60
DB 19 ITTGECTCPNLDQWQYDGHCVYASTYQVRWDAQLACQTVHPGAVLATIQSLENAFIS 78
QY 61 KFIENLLPSDGDGF-WIGLRREKQSNSTACQDLYAWTDGSIQSFRNMYVDEPS-----C 114
DB 79 ETYSN-----NRLWIGL-----NDILEGHVYWSNGEATDTYWSNNPNNWENQDC 125
QY 115 GSEVVCVVMYHQPAPAGIGGPFYFQWDDRCNNKNNFICK 154
DB 126 G-----VVDYTVTG-----QWDDDDCNKRNFLCK 151
RESULT 24
I50421
aggrecan precursor - chicken
N:Alternate names: cartilage chondroitin sulfate proteoglycan core protein
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C:Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072
J:Li, H.; Schwartz, N.B.; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A:Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
A:Reference number: A48884; MUID:94043149; PMID:8226978
A:Accession: I50421
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-2109 <LIX>
A:CROSS-references: GB:L21913; NID:g416133; PIDN:AAB19128.1; PID:g416134
R:Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 296, 885-887, 1993
A:Reference number: S39796; MUID:94107258; PMID:8280087
A:Contents: annotation; erratum
A:Accession: S39796
A:Molecule type: mRNA
A:Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1602, 'A'
A:CROSS-references: GB:M88101
R:Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 288, 903-910, 1992
A:Title: Molecular cloning of chicken aggregan. Structural analyses.
A:Reference number: S27356; MUID:93111968; PMID:1339285
A:Accession: S27356
A:Molecule type: mRNA
A:Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1549, 'T'
A:CROSS-references: EMBL:M88101
R:Sai, S.; Tanaka, T.; Koster, R.A.; Tanzer, M.L.
Proc. Natl. Acad. Sci. U.S.A. 83, 5081-5085, 1986
A:Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteoglyc
A:Reference number: A25442; MUID:86259736; PMID:3460082
A:Accession: A25442
A:Molecule type: mRNA
A:Residues: 1693-1795, 'G', 1797-1855, 1894-2109 <SAI>
A:CROSS-references: GB:M13993; NID:g211654; PIDN:AAA48720.1; PID:g211655
A:Experimental source: sternal cartilage
R:Ivanaka, T.; Har-El, R.; Tanzer, M.L.
J. Biol. Chem. 263, 15831-15835, 1988
A:Title: Partial structure of the gene for chicken cartilage proteoglycan core protein.
A:Reference number: A32002; MUID:89008500; PMID:3170613
A:Accession: A32002
A:Molecule type: DNA
A:Residues: 1893-1987, 'S', 1989-2022 <TAN>
A:Note: the authors translated the codon TCC for residue 1787 as Phe
R:Krueger, R.C.
J. Biol. Chem. 265, 12088-12097, 1990
A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide s
A:Reference number: I50216; MUID:90307744; PMID:1694853
A:Accession: I50216
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'PA', 1044-1559 <XRU>
A:CROSS-references: GB:M38187; NID:g211685; PIDN:AAA48731.1; PID:g555441
R:Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.
J. Biol. Chem. 265, 12075-12087, 1990
A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation an
A:Reference number: A37072; MUID:90307743; PMID:2365711
A:Accession: A37072
A:Molecule type: protein
A:Residues: 998-1015, 'X', 1017-1019, 'X', 1021-1023 <XR2>
A:Note: amino end of 86K core peptide CS-A
A:Accession: B37072
A:Molecule type: protein
A:Residues: 1247-1250, 'D', 1252-1272, 'X', 1274-1275 <XR3>
A:Note: amino end of 75K core peptide CS-B
C:Superfamily: aggregan; C-type lectin homology; complement factor H repeat homology; EG
C:Keywords: alternative splicing
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-2109/Product: aggregan #status predicted <MAT>
F:44-131/Domain: immunoglobulin homology <IMM>
F:166-243/Domain: link protein repeat homology <LNK1>
F:264-346/Domain: link protein repeat homology <LNK2>
F:537-614/Domain: link protein repeat homology <LNK3>
F:635-716/Domain: link protein repeat homology <LNK4>
F:1859-1890/Domain: EGF homology <EGF>
F:1897-2017/Domain: C-type lectin homology <LCH>
F:2024-2080/Domain: complement factor H repeat homology <FHD>

Query Match 13.2%; Score 146; DB 1; Length 2109;
Best Local Similarity 25.0%; Pred. No. 0.00021;
Matches 42; Conservative 28; Mismatches 58; Indels 40; Gaps 8;

Qy 15 ORPCYKVIYPHDTSRLNFFEEAKEACRRDGGQLVSISEDEQKLIKFIENLLPSDGF- 73
Db 1905 QGHCYR--HFEE---RETWMAESRCREHOAHLSITPPEQEFVNSHAQ-----DYQ 1952
Qy 74 WIGLRRERKQSNSTACODLYAWTDGSIQFRNYYVDEPS-----CGSEVCVVMYHQPAS 129
Db 1953 WIGLSDR-----AVENDFRMSDGHSLQFENWRNPQDNPFAGDCVVMWHEQG-- 2002
Qy 130 AGIGGPPYMFQWDRCKNMKNFTCKYS-----DEKPAVPSREASGEETE 173
Db 2003 -----EWNDVPCNYHLPTCKGTACGPPVVENARTFGRKND 2041
RESULT 25
JC7595
scavenger receptor with C-type lectin type I - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7595
R:Nakamura, K.; Funakoshi, H.; Miyamoto, K.; Tokunaga, F.; Nakamura, T.
Biochem. Biophys. Res. Commun. 280, 1028-1035, 2001
A:Title: Molecular cloning and functional characterization of a human scavenger receptor
A:Reference number: JC7595; MUID:21092718; PMID:11162630
A:Contents: Placenta
A:Accession: JC7595
A:Molecule type: mRNA
A:Residues: 1-742 <NAK>
A:CROSS-references: DDBJ:AB038518
C:Comment: This receptor, a member of the scavenger receptor family, belonging to the ty
important role in host defense. It forms a timer and plays a role in recognizing infect
C:Genetics:
A:Gene: srcl-1
A:Map position: 18p11.32
C:Keywords: coiled coil; glycoprotein; transmembrane protein
F:1-39/Domain: cytosolic (amino-terminus) #status predicted <CYT>
F:16-19/Region: internalization signal YKRF
F:40-56/Domain: transmembrane #status predicted <TM>
F:57-112/Domain: extracellular #status predicted <EXT>
F:113-335/Domain: coiled coil #status predicted <CC>
F:369-384/Region: serine/threonine-rich #status predicted
F:443-589/Domain: collagen-like #status predicted <COL>
F:607-732/Domain: C-type lectin/carbohydrate recognition domain #status predicted <CRD>
Query Match 13.2%; Score 145.5; DB 2; Length 742;
Best Local Similarity 28.7%; Pred. No. 6.9e-05;
Matches 39; Conservative 17; Mismatches 61; Indels 19; Gaps 5;
Qy 23 YFHDTSRLNFFEEAKEACRRDGGQLVSISEDEQKLIKFIENLLPSDGFWIGLRREE 82
Db 619 YFVSVEKEI-FEDAKGFCEDKSSHLVFINTRFQQWIKK-----QMVGRSHWIGLTDSR 673
Qy 83 QKSNSTACQDLYAWTDGSIQFRNYYVDEPSGSEVCVVMYHQPASAPAGIGGPPYMFQWND 142
Db 674 ENE-----WKWLDGTSPTYKNWAKAGQPDNNGH-----GHGPGEDCA-GLIYAGQWND 719
Qy 143 DRCKNMKNFTCKYSDE 158
Db 720 FQCEDVNNFICEKDRE 735

Search completed: September 9, 2004, 22:57:38
Job time : 26.0614 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:46:49 ; Search time 15.0369 Seconds
(without alignments)
706.418 Million cell updates/sec

Title: US-09-887-855-2_COPY_24_227

Perfect score: 1106

Sequence: 1 GRLLSGQPVCRGGTQRCYK.....BEDAKTKFKESREALNLAY 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	574	51.9	273	1	CHOD MOUSE
2	561.5	50.8	273	1	CHOD HUMAN
3	182	16.0	1456	1	MANR HUMAN
4	177	16.0	1268	1	PGCN MOUSE
5	176	15.9	1321	1	PGCN HUMAN
6	174.5	15.8	1381	1	PGCV BOVIN
7	174	15.7	1257	1	PGCV RAT
8	174	15.7	2738	1	PGCV RAT
9	174	15.7	3358	1	PGCV MOUSE
10	174	15.7	3396	1	PGCV HUMAN
11	171	15.5	3562	1	PGCV CHICK
12	165	14.9	643	1	C993 RAT
13	158.5	14.3	2364	1	PGCA BOVIN
14	158.5	14.3	2415	1	PGCA HUMAN
15	155.5	14.1	2333	1	PGCA CANFA
16	154.5	14.0	612	1	LEM2 MOUSE
17	153.5	13.9	644	1	C993 MOUSE
18	153.5	13.9	2124	1	PGCA RAT
19	152	13.7	912	1	PGCB BOVIN
20	151.5	13.7	652	1	C993 HUMAN
21	151	13.7	197	1	CLB1 HUMAN
22	149	13.5	321	1	FCB2 HUMAN
23	147.5	13.3	2132	1	PGCA MOUSE
24	147	13.3	883	1	PGCB MOUSE
25	146	13.2	2109	1	PGCA CHICK
26	145	13.1	158	1	LECG TRIST
27	145	13.1	883	1	PGCB RAT
28	144.5	13.1	173	1	LEC2 MEGRO
29	144.5	13.1	372	1	LEM1 RAT
30	143.5	13.0	372	1	LEM1 MOUSE
31	141.5	12.8	331	1	FCB2 MOUSE
32	141.5	12.8	549	1	LEM2 RAT
33	140.5	12.7	162	1	LEC3 MEGRO

34	140	12.7	370	1	LEM1 BOVIN
35	139	12.6	248	1	PSEA_HUMAN
36	139	12.6	283	1	LECA_SARPE
37	138.5	12.5	152	1	IXA TRIFL
38	138.5	12.5	202	1	TETN MOUSE
39	137.5	12.4	372	1	LEM1 MACMU
40	137.5	12.4	372	1	LEM1 PAPH
41	136	12.3	175	1	LITH_BOVIN
42	135	12.2	165	1	LITH_MOUSE
43	134.5	12.2	132	1	ACAL_ANGAN
44	134.5	12.2	372	1	LEM1_PONPY
45	134.5	12.2	485	1	LEM2_BOVIN

ALIGNMENTS

RESULT 1

CHOD MOUSE STANDARD; PRT; 273 AA.

AC QSCXMO: Q8VI31;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chondrolectin precursor (Transmembrane protein MT5)
GN CHODL.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Wang L., Smits P., Hubner R., Wouters J., Merregaert J.;
RT "Wt75, a low expressed c-type lectin gene involving in
chondrogenesis";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
Saito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
Schrml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Batsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.

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or send an email to license@isb-sib.ch).

EMBL; AF311699; AAL50354.1; -

DR EMBL; AK014255; BAB29226.1; --
DR HSP; P22897; 1EGG.
DR MGD; MG1:2179069; Chod1.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00411; C-TYPE LECTIN 2; 1.
KW Lectin; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 273 CHONDROLECTIN. (POTENTIAL).
FT DOMAIN 22 216 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 217 237 POTENTIAL.
FT DOMAIN 238 273 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 35 179 C-TYPE LECTIN.
FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 24 24 V -> W (IN REF. 2).
FT CONFLICT 179 179 T -> K (IN REF. 2).
SQ SEQUENCE 273 AA; 30303 MW; E052D933F244F4C7 CRC64;

Query Match 51.9%; Score 574; DB 1; Length 273;
Best Local Similarity 57.4%; Pred. No. 2.3e-44;
Matches 109; Conservative 26; Mismatches 41; Indels 14; Gaps 5;

QY 2 RLISGQVCRGCTQPCVKYVIFHDTSRLENFAKEACRRDGGOLVSIKLEK 61
DB 23 RVVSGQKCFADVHKPCYKAYFHELSRVSPQEARLACESEGGVLLSLENEASQKLES 82
QY 62 FIENLLP-----SDGFWIGLRREKQNSFACODLYAWTDGSGISQPRNRYVDEPSCGS 116
DB 83 MLQNLTKPGTSGDGFWIGLRLSGDGT-SGACPDLYQWSDGSSQPRNRYTDEPSCGS 141
QY 117 EVCVVMYHOPSPAGIGPYPQWQNDRCNKNFNICKYSDS-KPAVPSRAEGETELT 175
DB 142 EKVVMYHQTANPLGPGFYLQWQNDRCNKNFYCTYPEIHPTEPA-----EKPYLT 196
QY 176 TPVLPTEOTE 185
DB 197 NQ--PEETHE 204

RESULT 2
CHOD_HUMAN
ID CHOD_HUMAN STANDARD; PRT; 273 AA.
AC Q9HSP2; O9HCY3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Chondrolectin precursor (Transmembrane protein MT75) (Protein PRED12).
GN CHODL OR C21ORF68.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=20289799; PubMed=10830953;
RX MEDLINE=20289799; PubMed=12079284;
RA Weng L., Snits P., Wauters J., Metregaert J.;
RT "Molecular cloning and characterization of human chondrolectin, a novel type I transmembrane protein homologous to C-type lectins.";
RL Genomics 80:62-70(2002).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Tokoi Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudo J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordieck G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,

RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Liu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 27-273 FROM N.A.
RA Isoga T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
RA Wagaesuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP TISSUE SPECIFICITY.
RX MEDLINE=21564202; PubMed=11707072;
RA Raymond A., Friedli M., Neergard Henrichsen C., Chapot F., Deutsch S.,
RA Ucla C., Rossier C., Lyle R., Guipponi M., Antonarakis S.E.;
RT "From PREDs and open reading frames to cDNA isolation: revisiting the human chromosome 21 transcription map.";
RL Genomics 78:46-54(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Found in spleen, testis, prostate and fetal liver. Expression limited to vascular muscle of testis, smooth muscle of prostate stroma, heart muscle, skeletal muscle, crypts of small intestine, and red pulp of spleen.
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; AF257472; AAL05981.1; --
CC EMBL; AL163217; CAB90389.1; --
CC EMBL; BC009418; AAB09418.1; --
CC EMBL; AK022689; BAB14181.1; ALT_INIT.
CC HSP; P22897; 1EGG.
CC Genew; HGNC:17807; CHODL.
CC MIM; 607247; --
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.

-1-1-1 FUNCTION: Mediates the endocytosis of glycoproteins by macropinches, in several recognition and uptake processes.

-1-1 SUBCELLULAR LOCATION: Type I membrane protein.

-1-1 MISCELLANEOUS: CRDs 1-3 have at most very weak affinity for carbohydrate. CRD 4 shows the highest affinity binding and has multispecificity for a variety of monosaccharides. At least 3 CRDs (4, 5, and 7) are required for high affinity binding and endocytosis of multivalent glycoconjugates.

-1-1 SIMILARITY: Contains 8 C-type lectin family domains. .

-1-1 ID: Similarity: Contains 1 ricin B-type lectin domain.

-1-1 DATABASE: NAME=PROW; NLM=PROM 2:85-89(2001); WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1644341535_g.htm".

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EMBL; J05550; AAA59868.1; -.
ENMEL; M93221; AAA60389.1; -.
ENMEL; M93192; AAA60389.1; JOINED.
ENMEL; M93193; AAA60389.1; JOINED.
ENMEL; M93194; AAA60389.1; JOINED.
ENMEL; M93195; AAA60389.1; JOINED.
ENMEL; M93196; AAA60389.1; JOINED.
ENMEL; M93197; AAA60389.1; JOINED.
ENMEL; M93198; AAA60389.1; JOINED.
ENMEL; M93199; AAA60389.1; JOINED.
ENMEL; M93200; AAA60389.1; JOINED.
ENMEL; M93201; AAA60389.1; JOINED.
ENMEL; M93202; AAA60389.1; JOINED.
ENMEL; M93203; AAA60389.1; JOINED.
ENMEL; M93204; AAA60389.1; JOINED.
ENMEL; M93205; AAA60389.1; JOINED.
ENMEL; M93206; AAA60389.1; JOINED.
ENMEL; M93207; AAA60389.1; JOINED.
ENMEL; M93208; AAA60389.1; JOINED.
ENMEL; M93209; AAA60389.1; JOINED.
ENMEL; M93210; AAA60389.1; JOINED.
ENMEL; M93211; AAA60389.1; JOINED.
ENMEL; M93212; AAA60389.1; JOINED.
ENMEL; M93213; AAA60389.1; JOINED.
ENMEL; M93214; AAA60389.1; JOINED.
ENMEL; M93215; AAA60389.1; JOINED.
ENMEL; M93216; AAA60389.1; JOINED.
ENMEL; M93217; AAA60389.1; JOINED.
ENMEL; M93218; AAA60389.1; JOINED.
ENMEL; M93219; AAA60389.1; JOINED.
ENMEL; M93220; AAA60389.1; JOINED.
PIR; A36563; A36563.
PDB; 1EGG; 30-AUG-00.
PDB; 1EGI; 30-AUG-00.
NEW; HGNC:7228; MRC1.
MIM; 153618; -.
GO; GO:0005587; C:integral to plasma membrane; TAS.
GO; GO:0005537; F:mannose binding; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0006898; P:receptor mediated endocytosis; TAS.
InterPro; IPRO02353; AntifreezeII.
InterPro; IPRO00562; FN_type_II.
InterPro; IPRO01304; Lectin_C.
InterPro; IPRO00772; RicinB_lectin.
InterPro; IPRO08997; RicinB_Like.
fam; PF00040; fn2; 1.
fam; PF00059; lectin_c; 8.
fam; PF00652; RicinB_lectin; 2.
PRINTS; PR00356; ANTIFREEZEII.
PRINTS; PR00013; FNTYPEII.
ProDom; PD00095; FN_Type_II; 1.
SMART; SM00034; CLECT; 8.

DR SMART; SM00059; FN2: 1.
 DR SMART; SM00458; RICIN: 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; 6.
 DR PROSITE; PS00411; C-TYPE LECTIN 2; 8.
 DR PROSITE; PS00023; FIBRONECTIN 2; 1.
 DR PROSITE; PS00231; RICIN B LECTIN; 1.
 DR Receptor; Signal; Calcium-binding; Transmembrane; Repeat;
 KW Glycoprotein; Endocytosis; Macrophage; Lectin; Antigen; 3D-structure.
 FT SIGNAL 1 18
 FT CHAIN 19 1456
 FT DOMAIN 19 1393
 FT TRANSMEM 1384 1411
 FT DOMAIN 1412 1456
 FT DOMAIN 22 142
 FT DOMAIN 157 212
 FT DOMAIN 216 344
 FT DOMAIN 360 490
 FT DOMAIN 502 629
 FT DOMAIN 644 781
 FT DOMAIN 805 926
 FT DOMAIN 943 1083
 FT DOMAIN 1100 1216
 FT DOMAIN 1228 1359
 FT DISULFID 646 659
 FT DISULFID 680 777
 FT DISULFID 753 769
 FT CARBOHYD 104 104
 FT CARBOHYD 344 344
 FT CARBOHYD 529 529
 FT CARBOHYD 926 926
 FT CARBOHYD 930 930
 FT CARBOHYD 1160 1160
 FT CARBOHYD 1205 1205
 FT CARBOHYD 1311 1311
 FT TURN 648 649
 FT STRAND 651 652
 FT TURN 654 655
 FT STRAND 658 663
 FT HELIX 667 669
 FT STRAND 671 671
 FT HELIX 673 683
 FT TURN 684 684
 FT STRAND 686 687
 FT HELIX 693 705
 FT TURN 706 707
 FT TURN 709 710
 FT STRAND 712 718
 FT TURN 723 724
 FT STRAND 727 727
 FT TURN 729 730
 FT STRAND 733 733
 FT TURN 741 742
 FT STRAND 746 748
 FT STRAND 752 757
 FT TURN 758 761
 FT STRAND 764 768
 FT TURN 769 770
 FT STRAND 773 780
 FT TURN 781 782
 SQ SEQUENCE 1456 AA; 166011 MW; 2645EAF3C576A5E3 CRC64;
 Query Match 16.5%; Score 182; DB 1; Length 1456;
 Best Local Similarity 25.5%; Pred. No. 3.1e-08;
 Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;
 19 YKVIYFHTSRRLNFEAEKACRRDGGQLVSTESDEQKLEKFTENLLPSDGDWIGLR 78
 807 YKDYQYFYSKRETMNDAFCKRFGDLVLSQSSEKFLWKYV-NRNDQASVIFGLL 865
 79 RREKQSNSTACQDLVATWDGSGISQFRNWKVDEPSCGS--EVCVVMYHQPSPAGIGGPF 136
 866 ISLDKK-----FAWDGSKVDVSVATGEPFANEDNCVINY---SNSGF---- 908

QY 137 MFQWDDRCMNKNFTCKYSDK-----PAVPREAREGETELTTPVLPEETQE----- 185
 DB 909 ---WNDINGCYFNAPICQRHNSINATVMP-----TMPSPVSGCKEGWNFYSN 954
 QY 186 -----EDAKTKFKESREAL 200
 DB 955 KCFKIFGFMEERKNQWQEARAKCI 978
 RESULT 4
 PGCN_MOUSE STANDARD; PRT; 1268 AA.
 ID PGCN_MOUSE
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
 GN CSPG3 OR NCAN
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=96039250; PubMed=7490074;
 RA Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
 RA Faessler R.;
 RL "Structure and chromosomal localization of the mouse neurocan gene.";
 RL Genomics 28:405-410(1995).
 CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
 development by binding to neutral cell adhesion molecules (NG-CAM
 and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
 acid.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 2 link domains.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
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 or send an email to license@isb-sib.ch).
 CC EMBL; X84727; CAA59216.1; -.
 CC PIR; S52781; S52781.
 CC HSP; P00740; 1EDM.
 CC MGI; MGI:104694; CSPG3.
 CC InterPro; IPR002353; AntifreezeZell.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF 2.
 CC InterPro; IPR001881; EGF Ca.
 CC InterPro; IPR006209; EGF-like.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003599; Ig.
 CC InterPro; IPR001304; Lectin_C.
 CC InterPro; IPR000538; Link.
 CC InterPro; IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00059; lectin_c; 1.
 CC Pfam; PF00084; sushi_1.
 CC Pfam; PF00193; Xlink; 2.
 CC PRINTS; PR00356; ANTIFREEZEII.
 CC PRINTS; PR01265; LINKMODULE.
 CC ProDom; PD000918; Link; 2.
 CC SMART; SM00032; CCP; 1.

DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00445; LINK; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
 DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
 DR PROSITE; PS00022; EGF_1; 3.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS01241; LINK; 2.
 KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
 KW EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 1268
 FT DOMAIN 37 157
 FT DOMAIN 158 253
 FT DOMAIN 259 355
 FT DOMAIN 960 996
 FT DOMAIN 998 1034
 FT DOMAIN 1036 1165
 FT DOMAIN 1166 1224
 FT DISULFID 58 139
 FT DISULFID 181 252
 FT DISULFID 205 226
 FT DISULFID 279 354
 FT DISULFID 303 324
 FT DISULFID 964 975
 FT DISULFID 969 984
 FT DISULFID 986 995
 FT DISULFID 1040 1051
 FT DISULFID 1068 1160
 FT DISULFID 1136 1152
 FT DISULFID 1167 1210
 FT DISULFID 1196 1223
 FT CARBOHYD 121 121
 FT CARBOHYD 339 339
 FT CARBOHYD 742 742
 FT CARBOHYD 978 978
 FT CARBOHYD 1175 1175
 FT SEQUENCE 1268 AA; 137200 MW; 30148E202A2FAEC CRC64;

Query Match 16.0%; Score 177; DB 1; Length 1268;
 Best Local Similarity 31.5%; Pred. No. 7, 4e-08;
 Matches 45; Conservative 17; Mismatches 49; Indels 32; Gaps 6;

QY 15 QPCKVIYFHTSRRLNFEAKACRRDGGOLVSIKIEDEKQLEKFIENLLPSDGDWF 74
 Db 1048 QCHCYR--YF---AHRRWEDAECDRRRAGHLSVSPERKFINSP-----GHENSW 1096
 QY 75 IGLRREKQNSTACQDLYAWTDGSIQFRNYYVDEPS---CGSEVCVMYHQPAPAG 131
 Db 1097 IGLNDRTVRD-----PQWTDNTGLQYENWREKQDPNPFAGGDCVVMVAHESG--- 1145
 QY 132 TGGPYMFQWDDRCNMKNFNICK 154
 Db 1146 -----RWNDVPCYNLPYVCK 1161

RESULT 5
 PGCN_HUMAN
 ID PGCN_HUMAN STANDARD; PRT; 1321 AA.
 AC 014594; Q9UPK6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
 GN CSPG3 OR NCAN OR NEUR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99013874; PubMed=9795216;
 RA Prange C.K., Pennacchio L.A., Lieuallen K., Fan W., Lennon G.G.;
 RT "Characterization of the human neurocan gene, CSPG3.";
 RL Gene 221:199-205(1998).
 RN [2]
 RP SEQUENCE OF 1-990 AND 1007-1321 FROM N.A., AND VARIANT ALA-1254.
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Tetry A., Garnes J.,
 RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
 RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
 RA Coffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
 RA Kobayashi A., Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of an ~1 Mb region containing the MSP2B gene in
 19p12.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
 development by binding to neural cell adhesion molecules (NG-CAM
 and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
 acid.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 2 link domains.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF026547; AAC80576.1; -
 DR EMBL; AC003110; AAB86655.1; -
 DR EMBL; AC005254; AAC25581.1; -
 DR HSP; P00740; IEDM.
 DR Genew; HGNC:2465; CSPG3.
 DR MIM; 600826; -
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR000538; Link.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF00084; sushi; 1.
 DR Pfam; PF00193; Xlink; 2.
 DR PRINTS; PR01265; LINKMODULE.
 DR ProDom; PD000918; Link; 2.
 DR SMART; SMC0032; CCP; 1.
 DR SMART; SMC0034; CLECT; 1.
 DR SMART; SMC0179; EGF_CA; 1.
 DR SMART; SMC0409; IG; 1.
 DR SMART; SMC0445; LINK; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
 DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
 DR PROSITE; PS00022; EGF_1; 3.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 2.

DR PROSITE; PS01187; EGF CA; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 DR PROSITE; PS01241; LINK; 2.
 KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
 KW EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal; Polymorphism.
 FT SIGNAL 1 22
 FT CHAIN 23 1321
 FT DOMAIN 38 153
 FT DOMAIN 159 254
 FT DOMAIN 260 356
 FT DOMAIN 1008 1044
 FT DOMAIN 1046 1082
 FT DOMAIN 1084 1213
 FT DOMAIN 1214 1272
 FT DISULFID 59 140
 FT DISULFID 182 253
 FT DISULFID 206 227
 FT DISULFID 280 355
 FT DISULFID 304 325
 FT DISULFID 1012 1023
 FT DISULFID 1017 1032
 FT DISULFID 1034 1043
 FT DISULFID 1088 1099
 FT DISULFID 1116 1208
 FT DISULFID 1184 1200
 FT DISULFID 1215 1258
 FT DISULFID 1244 1271
 FT CARBOHYD 122 122
 FT CARBOHYD 340 340
 FT CARBOHYD 1026 1026
 FT CARBOHYD 1223 1223
 FT VARIANT 1254 1254
 FT CONFLICT 1234 1234
 FT CONFLICT 1282 1282
 FT SEQUENCE 1321 AA; 142972 MW; 2EF47F823DB980B8 CRC64;
 Query Match 15.9%; Score 176; DB 1; Length 1321;
 Best Local Similarity 31.5%; Pred. No. 9.6e-08;
 Matches 45; Conservative 18; Mismatches 48; Indels 32; Gaps 6;
 QY 15 QPCYKVIYFHTSRRLNPEAKACRRDGGOLGVSEDEOKLEKFIENLLPSDGF 74
 Db 1096 QGHCYR--YF---AHRAMEADAEKDCRRSGHLTSVHSPSEHSFNSE-----GHENTW 1144
 QY 75 IGLRREEQSNSTACQDIYANTDSISQFRNRYWYDEPS---CGSEVCVMVYHQPAPAG 131
 Db 1145 IGLNDRIVER-----FQMTDTGLQFENWRENQPDNFFAGGEDCVMVWVHESG--- 1193
 QY 132 IGGPYMFQWNRDRCKMKNFNICK 154
 Db 1194 -----RWNDVPCNVNLPYVCK 1209
 RESULT 6
 PGCV_BOVIN STANDARD; PRT; 3381 AA.
 AC P81282; 077609; 077610; 077611; 077612;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Vesican core protein precursor (large fibroblast proteoglycan)
 DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
 DE hyaluronate-binding protein) (GHAP).
 GN CP5G2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS VO; V1; V2 AND V3).
 RC TISSUE=Forebrain;

RX MEDLINE=98288320; PubMed=9624174;
 RA Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
 RA Zimmermann D.R.;
 RT "Vesican V2 is a major extracellular matrix component of the mature
 RT bovine brain.";
 RL J. Biol. Chem. 273:15758-15764 (1998).
 RP [2]
 RN SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
 RP AND 342-348.
 RC TISSUE=Spinal cord;
 RX MEDLINE=92062692; PubMed=1720020;
 RA Perides G., Biviano F., Bignami A.;
 RA "Interaction of a brain extracellular matrix protein with hyaluronic
 RT acid.";
 RL Biochim. Biophys. Acta 1075:248-258 (1991).
 CC -|- FUNCTION: May play a role in intercellular signaling and in
 CC connecting cells with the extracellular matrix. May take part in
 CC the regulation of cell motility, growth and differentiation. Binds
 CC hyaluronic acid.
 CC -|- SUBUNIT: Interacts with FBLN1 (By similarity).
 CC -|- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=V0;
 CC IsoId=P81282-1; Sequence=Displayed;
 CC Name=V1;
 CC IsoId=P81282-2; Sequence=VSP_003078; VSP_003079;
 CC Name=V2;
 CC IsoId=P81282-3; Sequence=VSP_003080;
 CC Name=V3;
 CC IsoId=P81282-4; Sequence=VSP_003081;
 CC -|- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed
 CC in the central nervous system, and in a number of mesenchymal and
 CC epithelial tissues; the major isoform V2 is restricted to the
 CC central nervous system.
 CC -|- DEVELOPMENTAL STAGE: Disappears after the cartilage development
 CC (By similarity).
 CC -|- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -|- SIMILARITY: Contains 2 link domains.
 CC -|- SIMILARITY: Contains 2 EGF-like domains.
 CC -|- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -|- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -|- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF060456; AAC24358.1; -;
 CC EMBL; AF060457; AAC24359.1; -;
 CC EMBL; AF060458; AAC24360.1; -;
 CC EMBL; AF060459; AAC24361.1; -;
 CC PIR; T14274; T14274.
 CC PIR; T42389; T42389.
 CC HSP; P01132; IEPG.
 CC InterPro; IPR000152; Asx_hydroxyl_s.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR000743; EGF_Ca.
 CC InterPro; IPR001881; EGF_Like.
 CC InterPro; IPR006209; EGF_Like.
 CC InterPro; IPR007110; Ig-Like.
 CC InterPro; IPR003599; Ig.
 CC InterPro; IPR001304; Lectin_C.
 CC InterPro; IPR000538; Link.
 CC InterPro; IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00059; Lectin_c; 1.
 CC Pfam; PF00084; sushi; 1.
 CC -----

DR PFam; PFO0193; Xlink; 2.
DR PRINTS; PRO1265; LINKMODULE.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C-TYPE LECTIN; 1.
DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG LINK; 1.
DR PROSITE; PS01241; LINK; 2.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 3381
FT DOMAIN 21 147
FT DOMAIN 168 245
FT DOMAIN 266 347
FT DOMAIN 349 1336
FT DOMAIN 1337 3074
FT DOMAIN 3074 3110
FT DOMAIN 3112 3148
FT DOMAIN 3161 3275
FT DOMAIN 3280 3338
FT DISULFID 44 131
FT DISULFID 173 244
FT DISULFID 197 218
FT DISULFID 271 346
FT DISULFID 295 316
FT DISULFID 3078 3089
FT DISULFID 3083 3098
FT DISULFID 3100 3109
FT DISULFID 3116 3127
FT DISULFID 3121 3136
FT DISULFID 3138 3147
FT DISULFID 3154 3165
FT DISULFID 3182 3274
FT DISULFID 3250 3266
FT DISULFID 3281 3324
FT DISULFID 3310 3337
FT CARBOHYD 57 57
FT CARBOHYD 331 331
FT CARBOHYD 352 352
FT CARBOHYD 817 817
FT CARBOHYD 965 965
FT CARBOHYD 1017 1017
FT CARBOHYD 1333 1333
FT CARBOHYD 1393 1393
FT CARBOHYD 1437 1437
FT CARBOHYD 1463 1463
FT CARBOHYD 1653 1653
FT CARBOHYD 1794 1794
FT CARBOHYD 2045 2045
FT CARBOHYD 2074 2074
FT CARBOHYD 2103 2103
FT CARBOHYD 2263 2263
FT CARBOHYD 2290 2290
FT CARBOHYD 2356 2356
FT CARBOHYD 2623 2623
FT CARBOHYD 2641 2641
FT CARBOHYD 2919 2919
FT CARBOHYD 3052 3052
FT CARBOHYD 3354 3354
FT CARBOHYD 3364 3364
FT VARSPLIC 349 349

PFam; PFO0193; Xlink; 2.
PRINTS; PRO1265; LINKMODULE.
ProDom; PD000918; Link; 2.
SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00615; C-TYPE LECTIN; 1.
PROSITE; PS00041; C-TYPE LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00026; EGF_3; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00835; IG LINK; 1.
PROSITE; PS01241; LINK; 2.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
Hyaluronic acid; Alternative splicing.
SIGNAL 1 20
CHAIN 21 3381
DOMAIN 21 147
DOMAIN 168 245
DOMAIN 266 347
DOMAIN 349 1336
DOMAIN 1337 3074
DOMAIN 3074 3110
DOMAIN 3112 3148
DOMAIN 3161 3275
DOMAIN 3280 3338
DISULFID 44 131
DISULFID 173 244
DISULFID 197 218
DISULFID 271 346
DISULFID 295 316
DISULFID 3078 3089
DISULFID 3083 3098
DISULFID 3100 3109
DISULFID 3116 3127
DISULFID 3121 3136
DISULFID 3138 3147
DISULFID 3154 3165
DISULFID 3182 3274
DISULFID 3250 3266
DISULFID 3281 3324
DISULFID 3310 3337
CARBOHYD 57 57
CARBOHYD 331 331
CARBOHYD 352 352
CARBOHYD 817 817
CARBOHYD 965 965
CARBOHYD 1017 1017
CARBOHYD 1333 1333
CARBOHYD 1393 1393
CARBOHYD 1437 1437
CARBOHYD 1463 1463
CARBOHYD 1653 1653
CARBOHYD 1794 1794
CARBOHYD 2045 2045
CARBOHYD 2074 2074
CARBOHYD 2103 2103
CARBOHYD 2263 2263
CARBOHYD 2290 2290
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CARBOHYD 2641 2641
CARBOHYD 2919 2919
CARBOHYD 3052 3052
CARBOHYD 3354 3354
CARBOHYD 3364 3364
VARSPLIC 349 349

FT VARSPLIC 350 1336
FT VARSPLIC 1337 3074
FT VARSPLIC 350 3074
FT VARSPLIC 350 3074
FT CONFLICT 25 25
FT CONFLICT 51 51
FT CONFLICT 89 96
FT CONFLICT 96 96
FT CONFLICT 346 346
FT CONFLICT 3381 AA; 369984 MW; F09716FA778D459 CRC64;
SQ SEQUENCE 3381 AA; 369984 MW; F09716FA778D459 CRC64;
Query Match 15.8%; Score 174.5; DB 1; Length 3381;
Best local similarity 25.3%; Pred. No. 4.2e-07;
Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;
QY 15 QRCYKVIYVPHDTSRLNPEEAKACRRDGGQLVSISEDEQKLIKFIENLLPSDGF- 73
DB 3162 QGQCYK--YF---AHRRTWDAERECRLQGAHLTSLSHHEEQMFVNRV-----GHDYQ 3209
QY 74 WIGLRRERKQSNSTACQDIYAWTDGSIQFRNYYVDEP-----SCSEVCVVMYHQPSP 129
DB 3210 WIGL-----NDKMFEDHDFRWDGTLQYENRNPQDPSFSTGDCVWIWHENG-- 3259
QY 130 AGIGGPFMFOWNDRCNMKNFKYKYS---DEKPAVPSREAEGE----- 170
DB 3260 -----QWNVPCNYHLTYTKGTGACGPPFVNAKTFGKMKPRYEINSLRYHC 3310
QY 171 -----ETELTT-----PVL-----PEETQEDAKTKFKESREALN 201
DB 3311 KDGFIQRHLPTIRCLNGRWAMPKITCLNPSAYQRTYSKKYKFNSSAKDN 3361
RESULT 7
ID PGCN RAT STANDARD; PRT; 1257 AA.
AC P55067;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
DE (245 kDa early postnatal core glycoprotein) [Contains: 150 kDa adult
DE core glycoprotein].
GN CSPG3 OR NCAN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
PP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=92406907; PubMed=1326557;
RA Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
RT "Cloning and primary structure of neurocan, a developmentally
RL regulated, aggregating chondroitin sulfate proteoglycan of brain.";
RN J. Biol. Chem. 267:19536-19547(1992).
[2]
RX CHARACTERIZATION.
RX MEDLINE=94230574; PubMed=7513709;
RA Friedlander D.R., Milev P., Karthikeyan L., Margolis R.K.,
RA Margolis R.U., Grumet W.;
RT "The neuronal chondroitin sulfate proteoglycan neurocan binds to the
RT neural cell adhesion molecules Ng-CAM/11/1NILE and N-CAM, and inhibits
RT neuronal adhesion and neurite outgrowth.";
RL J. Cell Biol. 125:669-680(1994).
CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
CC development by binding to neural cell adhesion molecules (NG-CAM
CC and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
CC acid.
CC -!- TISSUE SPECIFICITY: Early postnatal and adult brain; not expressed
CC in kidney, lung, liver and muscle.

CC -!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND
 CC O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
 CC -!- PTM: TWO ISOFORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC
 CC DEGRADATION. THE LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL
 CC BRAIN. THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
 CC
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 CC
 CC -----
 CC EMBL; M97161; AAC37679.1; -;
 CC PIR; S28764; S28764.
 CC HSP; P00740; IEDM.
 CC InterPro: IPR002353; Antifreeze2.
 CC InterPro: IPR000152; Asx hydroxyl_s.
 CC InterPro: IPR000742; EGF_2
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR006209; EGF_Like.
 CC InterPro: IPR007110; IG_Like.
 CC InterPro: IPR003599; IG.
 CC InterPro: IPR001304; Lectin_C.
 CC InterPro: IPR000538; Link.
 CC InterPro: IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00059; lectin_c; 1.
 CC Pfam; PF00084; sushi; 1.
 CC Pfam; PF00193; Xlink; 2.
 CC PRINTS; PR00356; ANTIFREEZE1.
 CC PRINTS; PR01245; LINKMODULE.
 CC ProDom; PD000918; Link; 2.
 CC SMART; SM00032; CCP; 1.
 CC SMART; SM00034; CLEC; 1.
 CC SMART; SM00179; EGF_CA; 1.
 CC SMART; SM00409; IG; 1.
 CC SMART; SM00445; LINK; 2.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
 CC PROSITE; PS00041; C-TYPE_LECTIN_2; 1.
 CC PROSITE; PS00022; EGF_1; 3.
 CC PROSITE; PS01186; EGF_2; 1.
 CC PROSITE; PS00026; EGF_3; 2.
 CC PROSITE; PS01187; EGF_CA; 1.
 CC PROSITE; PS00835; IG_LIKE; 1.
 CC PROSITE; PS0141; LINK; 2.
 CC
 CC KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
 CC EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
 CC
 CC SIGNAL 1 22
 CC FT CHAIN 23 1257 NEUCAN CORE PROTEIN.
 CC FT CHAIN 639 1257 150 kDa ADULT CORE GLYCOPROTEIN.
 CC FT DOMAIN 37 157 IG-LIKE V-TYPE.
 CC FT DOMAIN 158 233 LINK 1.
 CC FT DOMAIN 259 355 LINK 2.
 CC FT DOMAIN 949 985 EGF-LIKE 1.
 CC FT DOMAIN 987 1023 EGF-LIKE 2.
 CC FT DOMAIN 1025 1154 C-TYPE LECTIN.
 CC FT DOMAIN 1155 1213 SUSHI.
 CC FT DISULFID 58 139 BY SIMILARITY.
 CC FT DISULFID 181 222 BY SIMILARITY.
 CC FT DISULFID 205 226 BY SIMILARITY.
 CC FT DISULFID 279 354 BY SIMILARITY.
 CC FT DISULFID 303 324 BY SIMILARITY.
 CC FT DISULFID 953 964 BY SIMILARITY.

FT DISULFID 958 973 BY SIMILARITY.
 FT DISULFID 975 984 BY SIMILARITY.
 FT DISULFID 1029 1040 BY SIMILARITY.
 FT DISULFID 1057 1149 BY SIMILARITY.
 FT DISULFID 1125 1141 BY SIMILARITY.
 FT DISULFID 1156 1199 BY SIMILARITY.
 FT DISULFID 1185 1212 BY SIMILARITY.
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 737 737 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 944 944 O-LINKED (XYL. . .) (CHONDROITIN SULFATE).
 FT CARBOHYD 967 967 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1164 1164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1257 AA; 135544 MW; 992B33DCFAL9EE1B CRC64;
 Query Match 15.7%; Score 174; DB 1; Length 1257;
 Best Local Similarity 30.8%; Pred. No. 1.4e-07;
 Matches 44; Conservative 18; Mismatches 49; Indels 32; Gaps 6;
 Qy 15 QRCYKVIYFHDTSRLNFEAKEACRRDGGQGVSTSESEOKLEKFTENLLPSDGDWF 74
 Db 1037 QGHCYR--YF---AHRAWEDAECDRCRRAGHLSVHSPEEHKFINSF-----GHENSW 1085
 Qy 75 IGLRREKQSNSTACQDLYAMTDGSIQFRNMYVDEPS---CGSEVGVVMYHQPSAPAG 131
 Db 1086 IGLNDRTVED-----FQWTDNTGLQYENWREKQPDNFFAGGEDCVVMVAHENG--- 1134
 Qy 132 IGGPYMFWNDDECNMKNFICK 154
 Db 1135 -----RWDVPCNYNLPYVCK 1150

RESULT 8

PGCV RAT
 ID_PGCVRAT STANDARD; PRT; 2738 AA.
 AC Q9ERB4; O08592; O08564; Q9RIK4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Versican core protein precursor (large fibroblast proteoglycan)
 DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glia)
 DE hyaluronate-binding protein) (GHAP) (Fragments).
 GN CP5G2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 349-2738 FROM N.A. (ISOFORM V0), SEQUENCE FROM N.A.
 RP (ISOFORM V3), AND SEQUENCE OF 2657-2738 FROM N.A. (ISOFORM VINT).
 RC STRAIN=Wistar Kyoto;
 RX MEDLINE=9327053; PubMed=10397680;
 RA Lemire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
 RA Wight T.N.;
 RA "Versican/PG-M isoforms in vascular smooth muscle cells."
 RL Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
 RN [2]
 RP SEQUENCE OF 349-2738 FROM N.A. (ISOFORM V0).
 RC STRAIN=Wistar Kyoto;
 RX MEDLINE=98308094; PubMed=9642104;
 RA Milev P., Maurel P., Chiba A., Mevissen M., Popp S., Yamaguchi Y.,
 RA Margolis R.K., Margolis R.U.;
 RT "Differential regulation of expression of hyaluronan-binding
 RT proteoglycans in developing brain: aggrecan, versican, neurocan, and
 RT brevican."
 RL Biochem. Biophys. Res. Commun. 247:207-212(1998).
 RN [3]
 RP SEQUENCE OF 2421-2463 FROM N.A. (ISOFORM V0).
 RC TISSUE=Kidney;
 RX MEDLINE=98094159; PubMed=9434070;
 RA Pyke C., Kristensen P., Ostergaard P.B., Oturai P.S., Romer J.;
 RL "Proteoglycan expression in the normal rat kidney."
 RL Nephron 77:461-470(1997).

[4]
SEQUENCE OF 2535-2738 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE=Lung;
Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;
"Molecular cloning and characterization of two developmentally
regulated genes in rat lung";
Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: May play a role in intercellular signaling and in
connecting cells with the extracellular matrix. May take part in
the regulation of cell motility, growth and differentiation. Binds
hyaluronin acid.
-!- SUBUNIT: Interacts with FBLN1 (By similarity).
-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
Name=V0;
IsoId=Q9ERB4-1; Sequence=Displayed;
Name=V3;
IsoId=Q9ERB4-2; Sequence=VSP_003091;
Name=vint;
IsoId=Q9ERB4-3; Sequence=VSP_003092;
-!- TISSUE SPECIFICITY: In kidney is expressed in the papillary area,
but not in glomeruli.
-!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
(By similarity).
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

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or send an email to license@isb-sib.ch).

EMBL; AF062402; AAC40166.1; -;
EMBL; U75306; AAB51125.1; -;
EMBL; AF084544; AAD48544.1; -;
EMBL; AF072892; AAC26116.1; -;
EMBL; AV007691; AAG16631.1; -;
HSSP; P01132; 1EPG.
InterPro; IPR000152; Asx_hydroxyl_s.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR007110; IG-like.
InterPro; IPR003599; IG.
InterPro; IPR001304; Lectin_C.
InterPro; IPR00538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
PRINTS; PR01265; LINKMODULE.
ProDom; PD000918; Link; 2.
SMART; SM00034; CCP; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00615; C-TYPE LECTIN_1; 1.
PROSITE; PS00041; C-TYPE LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00026; EGF_3; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00835; IG LIKE; 1.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;

KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 2738 VERSICAN CORE PROTEIN.
FT NON CONS 348 349 IG-LIKE V-TYPE.
FT DOMAIN 21 146 LINK 1.
FT DOMAIN 167 244 LINK 2.
FT DOMAIN 265 346 GAG-ALPHA
FT DOMAIN <349 695 (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN).
FT DOMAIN 2431 GAG-BETA.
FT DOMAIN 2431 2467 EGF-LIKE 1.
FT DOMAIN 2469 2505 EGF-LIKE 2, CALCIUM-BINDING.
FT DOMAIN 2518 2632 C-TYPE LECTIN.
FT DOMAIN 2637 2695 SUSHI.
FT DISULFID 44 130 BY SIMILARITY.
FT DISULFID 172 243 BY SIMILARITY.
FT DISULFID 196 217 BY SIMILARITY.
FT DISULFID 270 345 BY SIMILARITY.
FT DISULFID 294 315 BY SIMILARITY.
FT DISULFID 2435 2446 BY SIMILARITY.
FT DISULFID 2440 2455 BY SIMILARITY.
FT DISULFID 2457 2466 BY SIMILARITY.
FT DISULFID 2473 2484 BY SIMILARITY.
FT DISULFID 2478 2493 BY SIMILARITY.
FT DISULFID 2495 2504 BY SIMILARITY.
FT DISULFID 2511 2522 BY SIMILARITY.
FT DISULFID 2539 2631 BY SIMILARITY.
FT DISULFID 2607 2623 BY SIMILARITY.
FT DISULFID 2638 2681 BY SIMILARITY.
FT DISULFID 2667 2694 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 692 692 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 758 758 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 802 802 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 805 805 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1257 1257 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1435 1435 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1633 1633 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1660 1660 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1684 1684 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1738 1738 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1848 1848 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2004 2004 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2409 2409 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2711 2711 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2721 2721 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 349 2431 Missing (in isoform V3).
FT VARSPLIC 2697 2738 /FTId=VSP_003091.
FT FT PSAYRTYRKYLKNGSSVVDNSINTSKHEHRSRRHQETR
FT FT R -> RQWSPKNGQPCFNKY (in isoform Vint).
FT FT /FTId=VSP_003092.
FT FT AEREK -> NSARG (in REF. 4).
FT CONFLICT 2535 2539
FT SEQUENCE 2738 AA; 300004 MW; 12CA626D58BD8C6A CRC64;

Query Match 15.7%; Score 174; DB 1; Length 2738;
Best Local Similarity 28.5%; Pred. No. 3.6e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;

Oy 15 QPCYKVIYFHTSRRLNFEAEACRRDGGQGVLSIESEDEQKLIKFIENLLPSDGF- 73
Db 2519 QGQYK--YF---AHRRTWDAARECLQAHITSLISHEEQMFVNEV-----GHDYQ 2566
Oy 74 WIGLRREEKQSNSTACQDLYAWTDGSIQFRWYVDEP-----SCGEVGVVWYHQSAP 129
Db 2567 WIGL-----NDKMFEDHFRWTDGSAQYENWRPNQDPDSFTSAGSDCVIIWHENG-- 2616
Oy 130 AGIGPYMFQWDDRCNNKNFKICKYS---DEKPAVPSREAGE 170
Db 2617 -----QWDDVPCNYHLTYTCKGTACGPPVVENAKTFGK 2652

RESULT 9
PGCV MOUSE STANDARD; PRT; 3358 AA.
AC O62059; Q62058; Q9CUU0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Versican core protein precursor (large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
GN CSPG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS V0; V1 AND V2).
RC STRAIN=C57BL/6, and Swiss Webster; TISSUE=Brain;
RX MEDLINE=95122551; PubMed=7822336;
RA Ito K., Shinomura T., Zako M., Ujita M., Kinata K.;
RT "Multiple forms of mouse PG-M, a large chondroitin sulfate
RT proteoglycan generated by alternative splicing.";
RL J. Biol. Chem. 270:958-965(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM V3).
RC STRAIN=C57BL/6;
RX MEDLINE=95181355; PubMed=7876137;
RA Zako M., Shinomura T., Ujita M., Ito K., Kinata K.;
RT "Expression of PG-M(V3), an alternatively spliced form of PG-M
RT without a chondroitin sulfate attachment in region in mouse and human
RT tissues.";
RL J. Biol. Chem. 270:3914-3918(1995).
RN [3]
RP SEQUENCE OF 1-1692 FROM N.A. (ISOFORM V1).
RC STRAIN=C57BL/6; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schrim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Gaasterland T., Gariboldi M., Gissi C., Forrest A., Frazer K.S.,
RA Daasterland T., Gariboldi M., Gissi C., Forrest A., Frazer K.S.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sangelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang X., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP INTERACTION WITH FBLN1.
RX MEDLINE=99329059; PubMed=10400671;
RA Asperger A., Adam S., Kostka G., Timpl R., Heinegaard D.;
RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
RT versican.";
RL J. Biol. Chem. 274:20444-20449(1999).
CC -!- FUNCTION: May play a role in intercellular signaling and in
connecting cells with the extracellular matrix. May take part in

the regulation of cell motility, growth and differentiation. Binds
hyaluronic acid.
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=Q62059-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=Q62059-2; Sequence=VSP_003087, VSP_003088;
CC Name=V2;
CC IsoId=Q62059-3; Sequence=VSP_003089;
CC Name=V3;
CC IsoId=Q62059-4; Sequence=VSP_003087, VSP_003090;
CC -!- TISSUE SPECIFICITY: V2 is found only in brain.
CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
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CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; D16263; BAA03796.1; -;
CC EMBL; D28599; -; NOT_ANNOTATED_CDS.
CC EMBL; D32040; BAA06802.1; -;
CC EMBL; AK014525; BAB29411.2; -;
CC HSP; P01132; 1EPG.
CC MGD; MGI:102889; Cspg2.
CC InterPro; IPR000152; Asx hydroxyl_1_s.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR007110; Ig-Like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 2.
CC PRINTS; PR01265; LINKMODULE.
CC PRODOM; PD000918; Link; 2.
CC SMART; SMC0032; CCP; 1.
CC SMART; SMC0034; CLEFT; 1.
CC SMART; SMC0179; EGF_CA; 1.
CC SMART; SMC0409; IG; 1.
CC SMART; SMC0445; LINK; 2.
CC PROSITE; PS00010; ASX HYDROXYL; 1.
CC PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
CC PROSITE; PS00041; C-TYPE_LECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS00026; EGF_3; 2.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 3358 VERSICAN CORE PROTEIN.

RC TISSUE=Brain;
 RX MEDLINE=89174663; PubMed=2466833;
 RA Perides G., Lane W.S., Andrews D., Dahl D., Bignami A.;
 RT "Isolation and partial characterization of a glial
 RT hyaluronate-binding protein";
 RL J. Biol. Chem. 264:5981-5987(1989).
 RN [9]
 RP TISSUE SPECIFICITY OF ISOFORMS.
 RX MEDLINE=96213482; PubMed=8627343;
 RA Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;
 RT "Differential expression of versican isoforms in brain tumors";
 RL J. Neuropathol. Exp. Neurol. 55:528-533(1996).
 CC -!- FUNCTION: May play a role in intercellular signaling and in
 CC connecting cells with the extracellular matrix. May take part in
 CC the regulation of cell motility, growth and differentiation. Binds
 CC hyaluronic acid.
 CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-5;
 CC Comment=Additional isoforms seem to exist;
 CC Name=V0;
 CC IsoId=PI3611-1; Sequence=Displayed;
 CC Name=V1;
 CC IsoId=PI3611-2; Sequence=VSP_003082, VSP_003083;
 CC Name=V2;
 CC IsoId=PI3611-3; Sequence=VSP_003084;
 CC Name=V3;
 CC IsoId=PI3611-4; Sequence=VSP_003082, VSP_003085;
 CC Name=Vint;
 CC IsoId=PI3611-5; Sequence=VSP_003086;
 CC -!- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed
 CC in normal brain, gliomas, medulloblastomas, schwannomas,
 CC neurofibromas, and meningiomas; V2 is restricted to normal brain
 CC and gliomas; V3 is found in all these tissues except
 CC medulloblastomas.
 CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 link domains.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U16306; AAG65018.1; -
 DR EMBL; X15988; AAB34128.1; -
 DR EMBL; S52488; AAB24978.1; -
 DR EMBL; U26555; AAA67565.1; -
 DR EMBL; D32039; BAA06801.1; -
 DR EMBL; J02814; AAA36437.1; -
 DR EMBL; AF084545; AAD48545.1; -
 DR PIR; S06014; A60979.
 DR HSSP; P01132; LEGF.
 DR Genew; HGNC:2464; CSPG2.
 DR MIM; 118661; -
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005540; F:hyaluronic acid binding; TAS.
 DR GO; GO:0008037; P:cell recognition; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR InterPro; IPR00152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.

DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR000538; Link.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF00084; sushi_1.
 DR Pfam; PF00193; Link; 2.
 DR PRINTS; PR01265; LINKMODULE.
 DR PRODom; PD000918; Link; 2.
 DR SMART; SM00032; CCP; 1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00409; IG_1.
 DR SMART; SM00445; LINK; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 DR PROSITE; PS00022; EGF_1_2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS01241; LINK; 2.
 KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
 KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
 KW Hyaluronic acid; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 3396
 FT DOMAIN 21 146
 FT DOMAIN 167 244
 FT DOMAIN 265 346
 FT DOMAIN 348 1335
 FT DOMAIN 1336 3089
 FT DOMAIN 3089 3125
 FT DOMAIN 3127 3163
 FT DOMAIN 3176 3290
 FT DOMAIN 3295 3353
 FT DISULFID 44 130
 FT DISULFID 172 243
 FT DISULFID 196 217
 FT DISULFID 270 345
 FT DISULFID 294 315
 FT DISULFID 3093 3104
 FT DISULFID 3098 3113
 FT DISULFID 3115 3124
 FT DISULFID 3131 3142
 FT DISULFID 3136 3151
 FT DISULFID 3153 3162
 FT DISULFID 3169 3180
 FT DISULFID 3197 3289
 FT DISULFID 3265 3281
 FT DISULFID 3296 3339
 FT DISULFID 3325 3352
 FT CARBOHYD 57 57
 FT CARBOHYD 330 330
 FT CARBOHYD 615 615
 Query Match 15.7%; Score 174; DB 1; Length 3396;
 Best Local Similarity 28.5%; Pred. No. 4.7e-07;
 Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
 QY 15 QRPCYVIYFHTSRLNFEFEAKEACRRDGGQGVLSIESDEBOKLEKFTENLLPSDGF- 73
 Db 3177 QGCYK--YF---AHERTWDAARECRLOGAHLTSLSHEEQMFVNRV-----GHYQ 3224
 QY 74 WIGLRRREKQSNSTACQDLYAVTWDSISQFNWYVDEP---SCGSEVCVVMHQPAP 129
 Db 3225 WIGL-----NDKMFEDHDFNTDGTSTLOYENWRPNQDSFFSAGEDCVIIWHNG--- 3274
 QY 130 AGIGGYPWFQWDDRCNMKNQNFICKYS-----DEKPAVPSREAGE 170
 Db 3275 -----QWNDVPCNVHLYTCKKGTVACGGPPVVENAKTFGK 3310

```

RESULT 11
PGCV CHICK
ID PGCV CHICK STANDARD; PRT; 3562 AA.
AC Q0953; Q0945;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Versican core protein precursor (large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
GN CPSG2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS V0 AND V1).
RC STRAIN=white leghorn; TISSUE=Limb bud;
RX MEDLINE=93300846; PubMed=8314802;
RA Shimomura T., Nishida Y., Ito K., Kinata K.;
RT "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan
RT expressed during chondrogenesis in chick limb buds. Alternative
RT spliced multiforms of PG-M and their relationships to versican.";
RL J. Biol. Chem. 268:14461-14469(1993).
CC -!- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=Q0953-1; Sequences=Displayed;
CC Name=V1;
CC IsoId=Q0953-2; Sequences=VSP 003093;
CC -!- TISSUE SPECIFICITY: Prechondrogenic condensation area of
CC developing limb buds.
CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC (By similarity).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X60226; CA442787.1; -
DR EMBL; D13542; BAA02742.1; -
DR PIR; A47171; A47171.
DR HSP; P00740; 1EDM.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001861; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.

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DR Pfam; PF00193; Xlink; 2.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLEF; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG_1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1_2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 26
FT CHAIN 27 3562
FT DOMAIN 27 143
FT DOMAIN 166 243
FT DOMAIN 264 345
FT DOMAIN 3254 3290
FT DOMAIN 3292 3328
FT DOMAIN 3341 3455
FT DOMAIN 3460 3518
FT DISULFID 44 129
FT DISULFID 171 242
FT DISULFID 195 216
FT DISULFID 269 344
FT DISULFID 293 314
FT DISULFID 3258 3269
FT DISULFID 3263 3278
FT DISULFID 3280 3289
FT DISULFID 3296 3307
FT DISULFID 3301 3316
FT DISULFID 3318 3327
FT DISULFID 3334 3345
FT DISULFID 3362 3454
FT DISULFID 3430 3446
FT DISULFID 3461 3504
FT DISULFID 3490 3517
FT CARBOHYD 163 163
FT CARBOHYD 235 235
FT CARBOHYD 329 329
FT CARBOHYD 529 529
FT CARBOHYD 709 709
FT CARBOHYD 948 948
FT CARBOHYD 1409 1409
FT CARBOHYD 1479 1479
FT CARBOHYD 1523 1523
FT CARBOHYD 1530 1530
FT CARBOHYD 1625 1625
FT CARBOHYD 1751 1751
FT CARBOHYD 1988 1988
FT CARBOHYD 2088 2088
FT CARBOHYD 2089 2089
FT CARBOHYD 2507 2507
FT CARBOHYD 2642 2642
FT CARBOHYD 2679 2679
FT CARBOHYD 2748 2748
FT CARBOHYD 2762 2762
FT CARBOHYD 3069 3069
FT CARBOHYD 3194 3194
FT CARBOHYD 3232 3232
FT CARBOHYD 3545 3545
FT VARSPPLIC 485 1411
SEQUENCE 3562 AA; 388078 MW; 9BC565E88C1602D2 CRC64;
/FTIG=VSP_003093.
Missing (in isoform V1).

```

Query Match 15.5%; Score 171; DB 1; Length 3562;
 Best Local Similarity 28.5%; Pred. No. 9.2e-07;
 Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
 QY 15 ORPCYKVIYHPTSRRLNFEAKACRRDGGOLVSIKLEKLEIENLLPSDGF- 73
 DB 3342 QOCYK--YF---AHRRTWDAERCRLOGAHLTSLSHGECVFNRI-----GHDIQ 3389
 QY 74 WIGLRREKQSNSTACQDLYATDGSISQFENWYVDEP---SCGSEVCVVMYHQPSAP 129
 DB 3390 WIGL-----NDKMFEDRFTDGSPLQYENWRPNQDPSFESAGEDCVVLIWHENG-- 3439
 QY 130 AGIGGYPYQWDDRCNMKNFICKYS-----DEKFAVPSREAGE 170
 DB 3440 -----QWNVPCNYHLTYTCKGTVACQGPVVENAKTFGK 3475

RESULT 12
 CD93_RAT STANDARD; PRT; 643 AA.
 AC Q9ET61; Q9JIZ6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Complement component C1q receptor precursor (Complement component 1, q subcomponent, receptor 1) (C1qR) (C1qR(p)) (C1q/MBL/SPA receptor)
 DE (CD93 antigen), receptor 1 (C1qR) (C1qR(p)) (C1q/MBL/SPA receptor)
 GN C1QR1 OR CD93 OR C1QRP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PVG; TISSUE=Natural killer cells;
 RX MEDLINE=20545218; PubMed=11093152;
 RA Lovik G., Vaage J.T., Dissen E., Szpirer C., Ryan J.C., Rolstad B.;
 RT "Characterization and molecular cloning of rat C1qR, a receptor on NK cells."
 RL Eur. J. Immunol. 30:3355-3362(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Lung;
 RX MEDLINE=20507883; PubMed=10934210;
 RA Dean Y.D., McGreal E.P., Akatsu H., Gasque P.;
 RT "Molecular and cellular properties of the rat A4 antigen, a C-type lectin-like receptor with structural homology to thrombospondin."
 RL J. Biol. Chem. 275:34382-34392(2000).
 CC -!- FUNCTION: Receptor (or element of a larger receptor complex) for C1q, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed. Highly expressed in lung and heart. Expressed at lower level in brain, thymus, liver, spleen, intestine, kidney, adrenal gland, muscle and testis. Expressed on endothelial cells, platelets, undifferentiated monocytes and circulating natural killer cells.
 CC -!- PTM: N- and O-glycosylated (By similarity).
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 5 EGF-like domains.
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 DR EMBL; AF136537; AAG01572.1; -;
 DR EMBL; AF160978; AAF80402.1; -;

HSP; P35555; IEMN.
 DR GO:0016021; C:integral to membrane; ISS.
 DR GO:0004872; F:receptor activity; ISS.
 DR GO:0016337; P:cell-cell adhesion; ISS.
 DR GO:0042116; P:macrophage activation; ISS.
 DR GO:0006809; P:phagocytosis; ISS.
 DR GO:0001152; ASX_hydroxyl_s.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR001304; LECTIN_C.
 DR Pfam; PF00008; EGF_4.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT_1.
 DR SMART; SM00179; EGF_CA; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3. FALSE_NEG.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
 KW EGF-like domain; Lectin; Glycoprotein.
 FT SIGNAL 1 23
 FT CHAIN 24 643
 FT DOMAIN 24 571
 FT TRANSMEM 572 592
 FT DOMAIN 593 643
 FT DOMAIN 31 173
 FT DOMAIN 257 298
 FT DOMAIN 299 341
 FT DOMAIN 342 381
 FT DOMAIN 382 423
 FT DOMAIN 424 462
 FT DISULFID 261 272
 FT DISULFID 268 282
 FT DISULFID 284 297
 FT DISULFID 303 314
 FT DISULFID 308 325
 FT DISULFID 327 340
 FT DISULFID 346 355
 FT DISULFID 351 364
 FT DISULFID 366 380
 FT DISULFID 386 397
 FT DISULFID 393 406
 FT DISULFID 408 422
 FT DISULFID 428 437
 FT DISULFID 433 446
 FT DISULFID 448 461
 FT CARBOHYD 322 322
 FT CARBOHYD 498 498
 FT CONFLICT 417 417
 SQ SEQUENCE 643 AA; 68781 MW; 9AE4C93AD943DB6 CRC64;
 Query Match 14.9%; Score 165; DB 1; Length 643;
 Best Local Similarity 25.2%; Pred. No. 3.8e-07;
 Matches 52; Conservative 35; Mismatches 73; Indels 46; Gaps 10;
 QY 1 GRLLSQGP-----VCRGGTQRCYKVIYHPTSRRLNFEAKACRRDGGOLVSIKSE 54
 DB 15 GQLWAGAAADSEAVVCEG---TACYTAHW-----GKLSAAEACHRGNGNLATYKSE 66
 QY 55 EQKLEKFIENLL-----PSD---GDSWIGLRREKQSNSTACQDLYATD---DGSISQFEN 106
 DB 67 EARRVQALQALQKTKAPSETKLGKWLQREKGTGKTHDLPKGFVWGGEDTYSN 126
 QY 107 WY-VDEPSCGSEVCVVMY-----HQPAPAGIGGYPYMFQWMDRC-----NMKNP 151
 DB 127 WYKASKSSCCSKKCVSLILDLSLKPHPSHLP-----KWHESPCTPDAPGNSIEGF 177
 QY 152 ICKYSDEKPAVPSREAGEETELTTP 177
 DB 178 LCKFNFKMGCSPLALGGPGLTYTTP 203

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RESULT 13
PGCA_BOVIN STANDARD; PRT; 2364 AA.
AC P13608; P79117; Q28159;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSPCP).
GN AGC1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eumetazoa; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hering T.M., Kollar J., Huynh T.D.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE OF 563-1056 FROM N.A.
RA MEDLINE=89380219; PubMed=2528543;
RX Oldberg A., Antonsson P., Heinegaard D., Oldberg A.;
RT "The keratan sulfate-enriched region of bovine cartilage proteoglycan
RT consists of a consecutively repeated hexapeptide motif.";
RN [3]
RP J. Biol. Chem. 264:16170-16173(1989).
RN [4]
RP SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
RX MEDLINE=87270630; PubMed=3111450;
RA Oldberg A., Antonsson P., Heinegaard D.;
RT "The partial amino acid sequence of bovine cartilage proteoglycan,
RT deduced from a cDNA clone, contains numerous Ser-Gly sequences
RT arranged in homologous repeats.";
RN [5]
RP Biochem. J. 243:255-259(1987).
RN [6]
RP SEQUENCE OF 2114-2150 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=93352525; PubMed=8349621;
RA Fueioep C., Walcz E., Valyon M., Glant T.T.;
RT "Expression of alternatively spliced epidermal growth factor-like
RT domains in aggregates of different species. Evidence for a novel
RT module.";
RN [7]
RP J. Biol. Chem. 268:17377-17383(1993).
RN [8]
RP PARTIAL SEQUENCE.
RX MEDLINE=85027710; PubMed=6489519;
RA Perin J.-P., Bonnet F., Jolles J., Jolles P.;
RT "Sequence data concerning the protein core of the cartilage
RT proteoglycan monomers. Characterization of a sequence allowing the
RT synthesis of an oligonucleotide probe.";
RN [9]
RP FEBS Lett. 176:37-42(1984).
RN [10]
RP PARTIAL SEQUENCE.
RX MEDLINE=8705253; PubMed=3530809;
RA Perin J.P., Bonnet F., Jolles P.;
RT "Structural relationship between link proteins and proteoglycan
RT monomers.";
RN [11]
RP FEBS Lett. 206:73-77(1986).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
CC matrix of cartilaginous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an amino-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=alternative splicing; Named isoforms=2;
CC Name=1;
CC isoId=P13608-1; Sequence=Displayed;
CC Name=2;
CC isoId=P13608-2; Sequence=VSP_003072;
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
terminus of the proteoglycan, while another globular region, G3,
makes up the C-terminus. G1 contains link domains and thus
consists of three disulfide-bonded loop structures designated as
the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
and the chondroitin sulfate (CS) attachment domains lie between G2
and G3.
CC -!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-
LINKED (ABOUT 40) OLIGOSACCHARIDES.
CC -!- PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN
ADULT AND FETAL BOVINE PROTEOGLYCANS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
-----
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or send an email to license@isb-sib.ch).
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CC EMBL; U76615; AAB38524.1; -.
CC EMBL; L07053; -. NOT_ANNOTATED_CDS.
CC PIR; A34234; A33808.
CC PIR; T42830; T42630.
CC HSP; P08709; IBF9.
CC InterPro; IPR002353; Antifreeze1.
CC InterPro; IPR000152; Asx hydroxyl_s.
CC InterPro; IPR000742; EGF-2.
CC InterPro; IPR001881; EGF-Ca.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR003324; SGXSG.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 1.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF02339; SGXSG; 61.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 4.
CC PRINTS; PR00356; ANTIFREEZE1I.
CC PRINTS; PR0265; LINKMODULE.
CC PRODOM; PD000918; Link; 4.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00445; LINK; 4.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS00026; EGF_3; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00290; IG_MHC; FALSE_NEG.
CC PROSITE; PS01241; LINK; 4.
CC GlycoProfile; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
KW GlycoProfile; Repeat; Immunoglobulin domain.
FT SIGNAL 1 16
FT CHAIN 17 2364 AGGREGAN CORE PROTEIN.
FT DOMAIN 25 147 IG-LIKE V-TYPE.
FT DOMAIN 170 247 LINK 1.
FT DOMAIN 268 349 LINK 2.
FT DOMAIN 504 581 LINK 3.
FT DOMAIN 602 683 LINK 4.
FT DOMAIN 774 907 23 X 6 AA APPROXIMATE TANDEM REPEATS OF
```


regulatory role in the matrix assembly of the cartilage.
 -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).
 -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino terminus of the proteoglycan, while another globular region, G3, makes up the COOH terminus. G1 contains link domains and thus consists of three disulfide-bonded loop structures designated as the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS) and the chondroitin sulfate (CS) attachment domains lie between G2 and G3.
 -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate chains. N-linked and O-linked oligosaccharides (By similarity).
 -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 -!- SIMILARITY: Contains 4 link domains.
 -!- SIMILARITY: Contains 1 C-type lectin family domain.
 -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 -!- SIMILARITY: Contains 1 EGF-like domain.
 -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

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 EMBL; U65989; AAB06238.2; -
 DR EMBL; S74662; AAC60527.1; -
 DR EMBL; L07054; -; NOT ANNOTATED_CDS.
 DR PIR; I46998; I46998.
 DR HSP; P08709; 1BP9.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR000152; Asx hydroxyl_s.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR000538; Link.
 DR InterPro; IPR003324; SGXSG.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF02339; SGXSG; 66.
 DR Pfam; PF00084; sushi; 1.
 DR Pfam; PF00193; Xlink; 4.
 DR PRINTS; PR00356; ANTIFREEZEII.
 DR PRINTS; PR01265; LINKMODULE.
 DR ProDom; PD000918; Link; 4.
 DR SMART; SM00032; CCP; 1.
 DR SMART; SM00034; CLEC; 1.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00445; LINK; 4.
 DR PROSITE; PS00010; ASX HYDROXYL; 1.
 DR PROSITE; PS00615; C TYPE LECTIN; 1.
 DR PROSITE; PS0041; C TYPE LECTIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS01241; LINK; 4.
 KW Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
 KW Repeat; Immunoglobulin domain.
 FT SIGNAL; 16
 FT CHAIN; 17 2333
 FT DOMAIN; 34 147
 FT DOMAIN; 170 247
 FT DOMAIN; 268 349
 FT DOMAIN; 513 590
 FT LINK 1.
 FT LINK 2.
 FT LINK 3.
 FT POTENTIAL.
 FT AGGREGAN CORE PROTEIN.
 FT IG-LIKE V-TYPE.
 FT LINK 1.
 FT LINK 2.
 FT LINK 3.

FT DOMAIN; 611 692
 FT DOMAIN; 2081 2117
 FT DOMAIN; 2130 2245
 FT DOMAIN; 2249 2307
 FT DOMAIN; 48 140
 FT DOMAIN; 152 247
 FT DOMAIN; 253 349
 FT DOMAIN; 495 589
 FT DOMAIN; 596 691
 FT DOMAIN; 694 816
 FT DOMAIN; 819 1394
 FT DOMAIN; 1395 2079
 FT DOMAIN; 2080 2333
 FT DISULFID; 51 133
 FT DISULFID; 175 246
 FT DISULFID; 199 220
 FT DISULFID; 273 348
 FT DISULFID; 297 318
 FT DISULFID; 518 589
 FT DISULFID; 542 563
 FT DISULFID; 616 691
 FT DISULFID; 640 661
 FT DISULFID; 2085 2096
 FT DISULFID; 2090 2105
 FT DISULFID; 2107 2116
 FT DISULFID; 2123 2134
 FT DISULFID; 2151 2243
 FT DISULFID; 2219 2235
 FT DISULFID; 2250 2293
 FT DISULFID; 2279 2306
 FT CARBOHYD; 126 126
 FT CARBOHYD; 239 239
 FT CARBOHYD; 333 333
 FT CARBOHYD; 387 387
 FT CARBOHYD; 444 444
 FT CARBOHYD; 620 620
 FT CARBOHYD; 676 676
 FT CARBOHYD; 747 747
 SQ SEQUENCE 2333 AA; 240573 MW; 8B9ED78F3508B596 CRC64;
 Query Match 14.1%; Score 155.5; DB 1; Length 2333;
 Best Local Similarity 28.5%; Pred. No. 1.3e-05;
 Matches 51; Conservative 24; Mismatches 61; Indels 43; Gaps 11;
 Qy 7 QPVCRG--TQPCYKVIYFHTSRLNFEAKEACRRDGGQLVSIEDSKLIEFI 63
 Db 2120 QELCEGWTKFQGHCVR--YFPD---RESWVDAESRCRAQQSHLSIVTPEQ---EFV 2170
 Qy 64 ENLLPSDGP-WTGLRRREKQSNSTACQDLVATDGSISQFNWYVDPS---CGSEVC 119
 Db 2171 NN---NAQYQWIGL-----NDRTIEGDFWSDGHSLOFNWRPNQDFVSGEDC 2219
 Qy 120 VVM-YHQPSAPAGIGPYFQWNRDRCNMKNFICKYS----DEKPAVPSRAEGETE 173
 Db 2220 VVMWHEKG-----EMWDFVCNYLPTCKKGTGACGDPVWEHARTFGQKD 2267
 RESULT 16
 LEM2 MOUSE
 ID LEM2 MOUSE STANDARD; PRT; 612 AA.
 AC Q00650;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
 DE (ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM2).
 GN SELE OR ELAM-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=92283265; PubMed=1375914;
RA Becker-Andre M., van Huijsduijn R.H., Losberger C., Whelan J.,
RA Delamarre J.F.;
RT "Murine endothelial leukocyte-adhesion molecule 1 is a close
RT structural and functional homologue of the human protein.";
RL Eur. J. Biochem. 206:401-411(1992).
RN [2].
RP SEQUENCE FROM N.A.
RX MEDLINE=92340571; PubMed=1378846;
RA Welher A., Isenmann S., Vestweber D.;
RT "Cloning of the mouse endothelial selectins. Expression of both E-
RT and P-selectin is inducible by tumor necrosis factor alpha.";
RL J. Biol. Chem. 267:15176-15183(1992).
CC -!- FUNCTION: Expressed on cytokine induced endothelial cells and
CC mediates their binding to leukocytes. The ligand recognized by
CC ELAM-1 is sialyl-Lewis X (alpha(1-3)fucosylated derivatives of
CC polyactosamine that are found at the nonreducing terminus of
CC glycolipids).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the selectin/LECAM family.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 6 Sushi (SCR) domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M80778; AAA37547.1; .
DR EMBL; M87862; AAA37577.1; ALT_INIT.
DR PIR; S23174; B42755.
DR HSP; F16581; IKAJ.
DR MGD; MGI:98278; Sele.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR002396; Selectin.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 6.
DR PRINTS; PR00343; SELECTIN.
DR SMART; SM00032; CCP; 6.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS00441; C-TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS50026; EGF 3; 1.
KW Cell adhesion, Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 612 E-SELECTIN.
FT DOMAIN 22 557 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 558 579 POTENTIAL.
FT DOMAIN 580 612 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 139 C-TYPE LECTIN.
FT DOMAIN 140 175 EGF-LIKE.
FT DOMAIN 179 239 SUSHI 1.
FT DOMAIN 242 301 SUSHI 2.
FT DOMAIN 304 364 SUSHI 3.
FT DOMAIN 367 427 SUSHI 4.
FT DOMAIN 430 490 SUSHI 5.
FT DOMAIN 493 549 SUSHI 6.
FT DISULFID 40 138 BY SIMILARITY.
FT DISULFID 111 130 BY SIMILARITY.
FT DISULFID 143 154 BY SIMILARITY.
FT DISULFID 148 163 BY SIMILARITY.

FT DISULFID 165 174 BY SIMILARITY.
FT DISULFID 180 225 BY SIMILARITY.
FT DISULFID 210 238 BY SIMILARITY.
FT DISULFID 243 287 BY SIMILARITY.
FT DISULFID 273 300 BY SIMILARITY.
FT DISULFID 305 350 BY SIMILARITY.
FT DISULFID 336 363 BY SIMILARITY.
FT DISULFID 368 413 BY SIMILARITY.
FT DISULFID 399 426 BY SIMILARITY.
FT DISULFID 431 476 BY SIMILARITY.
FT DISULFID 462 489 BY SIMILARITY.
FT DISULFID 494 535 BY SIMILARITY.
FT DISULFID 521 548 BY SIMILARITY.
FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 504 504 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 528 528 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 612 AA; 66749 MW; 86F05713F0EC2C3D CRC64;
Query Match 14.0%; Score 154.5; DB 1; Length 612;
Best Local Similarity 27.9%; Pred. No. 3.2e-06;
Matches 38; Conservative 28; Mismatches 45; Indels 25; Gaps 5;
Qy 23 YFHTSRRLNFERAKACRRDGGQLVSIIESDSQKUIEKFIENLLPSDGFWTGLRRRE 82
Db 23 YNASSSLMTYDEASAYCQRDYTHLVAIQNKEE---INYLNSLNKHSYVYGIK-- 76
Qy 83 KQSNSTACQDLXAWTDGS---ISQFRNYYVDPS---CGSEVCVVMYHOPAPAGIGGPPYM 137
Db 77 -----VNNVWLVVGTGKPLTEEAQNAPGEPNNKQRNEDCCEVIYIQTQDSGM----- 124
Qy 138 FQWDDRCNNMKNFIC 153
Db 125 --WNDERCNKKLALC 138
RESULT 17
CD93 MOUSE STANDARD; PRT; 644 AA.
AC 089103;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Complement component C1q receptor precursor (Complement component 1, q
DE subcomponent, receptor 1) (C1qR) (C1qR(p)) (C1g/MBL/SPA receptor)
DE (CD93 antigen) (Cell surface antigen AA4) (Lymphocyte antigen 68).
GN C1QR1 OR CD93 OR C1QRP OR LY68 OR AA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV;
RC MEDLINE=20528605; PubMed=11074255;
RA Kim T.S., Park M., Nepomuceno R.R., Palmarini G., Winokur S.,
RA Cotman C.A., Bengtsson U., Tenner A.J.;
RT "Characterization of the murine homolog of C1qR(p): identical cellular
RT expression pattern, chromosomal location and functional activity of
RL the human and murine C1qR(p).";
RN Mol. Immunol. 37:377-389(2000).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukemia;
RX MEDLINE=99330438; PubMed=10403644;
RA Petrenko O., Beavis A., Klaine M., Kittappa R., Godin I.,
RA Lemischka I.R.;
RT "The molecular characterization of the fetal stem cell marker AA4.";

Immunity 10:691-700 (1999).

[3]

SEQUENCE FROM N.A.

STRAIN=129/SV; TISSUE=Endothelial cells, and Spleen;

MEDLINE=99359842; PubMed=10430665;

Norworthy P.J., Taylor P.R., Walport M.J., Botto M.;

"Cloning of the mouse homolog of the 126-kDa human C1q/MBL/SP-A receptor, Clqrp."

Mamm. Genome 10:789-793 (1999).

CC -!- FUNCTION: Receptor (or element of a larger receptor complex) for C1q, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SP). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion. Marker for early multipotent hematopoietic precursor cells. May play a role in cell-cell interactions during hematopoietic and vascular development.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed in lung, heart and bone marrow. Expressed at lower level in ovary, whole embryo and fetal liver. Not detected in brain, adult liver or thymus. Highly expressed in peritoneal cavity and bone marrow macrophages. Not detected in epithelial cells.

CC -!- DEVELOPMENTAL STAGE: First detectable in day 9 embryos, in the endocardium and vascular endothelium in the anterior part of the embryo. Expression in endothelial cells, initially restricted to aorta, omphalomesenteric and umbilical arteries, later extends to subcardinal veins, intersomitic arteries and perineural vessels.

CC On day 10, detectable in the entire embryo.

CC -!- PTM: N- and O-glycosylated (By similarity).

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

CC -!- SIMILARITY: Contains 5 EGF-like domains.

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CC -----

CC EMBL; AF074856; AAC63274.1; -.

CC EMBL; AF081789; AAC62649.1; -.

CC EMBL; AF099939; AAD47906.1; -.

CC EMBL; AF099938; AAD47906.1; JOINED.

CC HSSP; P35555; 1EWN.

CC MGD; MG1:106664; Clqrl.

CC GO; GO:0016023; C:cytoplasmic vesicle; IDA.

CC GO; GO:0016021; C:integral to membrane; ISS.

CC GO; GO:0005886; C:plasma membrane; IDA.

CC GO; GO:0004872; F:receptor activity; ISS.

CC GO; GO:0016337; P:cell-cell adhesion; ISS.

CC GO; GO:0042116; P:macrophage activation; ISS.

CC GO; GO:0006909; P:phagocytosis; ISS.

CC InterPro; IPR001152; ASX_hydroxyl_S.

CC InterPro; IPR001881; EGF_Ca.

CC InterPro; IPR006209; EGF-like.

CC InterPro; IPR001304; Lectin_C.

CC Pfam; PF00008; EGF; 5.

CC Pfam; PF00059; lectin_c; 1.

CC SMART; SM00034; CLECT; 1.

CC SMART; SM00179; EGF_CA; 3.

CC PROSITE; PS00010; ASX_HYDROXYL; 3.

CC PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.

CC PROSITE; PS50041; C-TYPE LECTIN_2; 1.

CC PROSITE; PS01186; EGF_2; 3.

CC PROSITE; PS50026; EGF_3; 4.

CC PROSITE; PS01187; EGF_CA; 3.

CC Cell adhesion; Receptor; Repeat; Signal; Transmembrane; EGF-like domain; Lectin; Glycoprotein.

KW SIGNAL

FT CHAIN 1 22 POTENTIAL.

FT CHAIN 23 644 COMPLEMENT COMPONENT C1Q RECEPTOR.

FT DOMAIN 23 572 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	573	593	POTENTIAL.
FT	DOMAIN	594	644	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	31	173	C-TYPE LECTIN.
FT	DOMAIN	257	298	EGF-LIKE 1.
FT	DOMAIN	299	341	EGF-LIKE 2.
FT	DOMAIN	342	381	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	382	423	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	424	465	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DISULFID	261	272	BY SIMILARITY.
FT	DISULFID	268	282	BY SIMILARITY.
FT	DISULFID	284	297	BY SIMILARITY.
FT	DISULFID	303	314	BY SIMILARITY.
FT	DISULFID	308	325	BY SIMILARITY.
FT	DISULFID	327	340	BY SIMILARITY.
FT	DISULFID	346	355	BY SIMILARITY.
FT	DISULFID	351	364	BY SIMILARITY.
FT	DISULFID	366	380	BY SIMILARITY.
FT	DISULFID	386	397	BY SIMILARITY.
FT	DISULFID	393	406	BY SIMILARITY.
FT	DISULFID	408	422	BY SIMILARITY.
FT	DISULFID	428	440	BY SIMILARITY.
FT	DISULFID	436	449	BY SIMILARITY.
FT	DISULFID	451	464	BY SIMILARITY.
FT	CARBOHYD	102	102	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	322	322	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	644 AA;	69354 MW;	EB4351648BF8635A CRC64;

Query Match 13.9%; Score 153.5; DB 1; Length 644;

Best Local Similarity 24.1%; Pred. No. 4.1e-06;

Matches 51; Conservative 32; Mismatches 70; Indels 59; Gaps 11;

Qy 4 LSCQP-----VCRGGTQPCYKVIYFHTSRRLNFEAKACRRDGGQLVSIES 52

Db 13 LLGPGWAGAAADQAVVCEG---TACYTAHW-----GKLSAAEAQRCNENGSLATVKS 64

Qy 53 EDQKLIKFIENLPSD-----GDFWGLRRREKQSNSTACDL---YAVT-DGS 100

Db 65 EEARHVQQLTQLTKKAPLEAKMGKFWIGLQK---EKGCTYHDLPMRGFSGVGGE 120

Qy 101 ISGFPRNYY-VDEPSCGSEVCCVVMY-----HPSAPAGIGGYPQWMDRC----- 145

Db 121 DTAYSNNYKASKSCIFKRCVSLDLSLTPHSLP-----KWHESFCGTPEAPG 171

Qy 146 NMKNFICKYSDKPAVPSREAGEETELTP 177

Db 172 NSIEGLCKFNFKMCRPLALGGPGRVYVTP 203

RESULT 18

PGCA_RAT	STANDARD;	PRT;	2124 AA.
ID PGCA_RAT			
AC P07897;			
DT 01-AUG-1988 (Rel. 08, Created)			
DT 01-FEB-1991 (Rel. 17, Last sequence update)			
DT 15-MAR-2004 (Rel. 43, Last annotation update)			
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSFPCP).			
GN AGC1 OR AGC.			
OS Rattus norvegicus (Rat).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX NCBI_TaxID=10116;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=8087070; PubMed=3693370;			
RA Doerge K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;			
RT "Complete primary structure of the rat cartilage proteoglycan core protein deduced from cDNA clones."			
RL J. Biol. Chem. 262:17757-17767(1987).			
RN [2]			
RP REVISION TO 598.			
RA Doerge K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;			
RL J. Biol. Chem. 263:10040-10040(1988).			

[3]
RN SEQUENCE OF 1856-2124 FROM N.A.
RX MEDLINE=86250898; PubMed=2424893;
RA Doegge K., Fernandez P., Hassell J.R., Sasaki M., Yamada Y.;
RT "partial cDNA sequence encoding a globular domain at the C terminus
of the rat cartilage proteoglycan";
RL J. Biol. Chem. 261:8108-8111(1986).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
matrix of cartilaginous tissues. A major function of this protein
is to resist compression in cartilage. It binds avidly to
hyaluronic acid via an amino-terminal globular region. May play a
regulatory role in the matrix assembly of the cartilage.
CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
similarity).
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
terminus of the proteoglycan, while another globular region, G3,
makes up the COOH terminus. G1 contains link domains and thus
consists of three disulfide-bonded loop structures designated as
the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
and the chondroitin sulfate (CS) attachment domains lie between G2
and G3.
CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
chains, N-linked and O-linked oligosaccharides.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M13518; AAA41836.1; -
CC EMBL; J03485; AAA21000.1; ALT_SEQ.
CC PIR; A92623; A28452.
CC HSP; P98066; 1TSG.
CC InterPro; IPR002353; Antifreeze1.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR003324; SGXSG.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00047; Ig_1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF02339; SGXSG; 55.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 4.
CC PRINTS; PR00356; ANTIFREEZE1.
CC PRINTS; PR01285; LINKMODULE.
CC ProDom; PD000918; Link; 4.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00406; IGV; 1.
CC SMART; SM00445; LINK; 4.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
CC PROSITE; PS00441; C_TYPE_LECTIN_2; 1.
CC PROSITE; PS00835; IG-LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC PROSITE; PS01241; LINK; 4.
KW Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; Repeat;
KW Immunoglobulin domain.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 2124 AGGECAN CORE PROTEIN.
FT DOMAIN 34 147 IG-LIKE V-TYPE.
FT DOMAIN 170 247 LINK 1.

DOMAIN 268 349
FT DOMAIN 504 581 LINK 2.
FT DOMAIN 602 683 LINK 3.
FT DOMAIN 1910 2036 C-TYPE LECTIN.
FT DOMAIN 2040 2098 SUSHI.
FT DOMAIN 48 140 G1-A.
FT DOMAIN 152 247 G1-B.
FT DOMAIN 253 349 G1-B'.
FT DOMAIN 486 580 G2-B.
FT DOMAIN 587 682 G2-B'.
FT DOMAIN 685 798 KS.
FT DOMAIN 801 1226 CS-1.
FT DOMAIN 1227 1909 CS-2.
FT DOMAIN 1910 2124 G3.
FT DISULFID 51 133 BY SIMILARITY.
FT DISULFID 175 245 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT DISULFID 273 348 BY SIMILARITY.
FT DISULFID 297 318 BY SIMILARITY.
FT DISULFID 509 580 BY SIMILARITY.
FT DISULFID 533 554 BY SIMILARITY.
FT DISULFID 607 682 BY SIMILARITY.
FT DISULFID 631 652 BY SIMILARITY.
FT DISULFID 1914 1925 BY SIMILARITY.
FT DISULFID 1942 2034 BY SIMILARITY.
FT DISULFID 2010 2026 BY SIMILARITY.
FT DISULFID 2041 2084 BY SIMILARITY.
FT DISULFID 2070 2097 BY SIMILARITY.
FT CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 667 667 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1842 1842 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 2124 AA; 221117 MW; E30BB561593A34B1 CRC64;

Query Match 13.9%; Score 153.5; DB 1; Length 2124;
Best Local Similarity 26.3%; Pred. No. 1.8e-05;
Matches 47; Conservative 27; Mismatches 62; Indels 43; Gaps 9;

Qy 7 QPVCGRG---TORPCYKVIYFHDTSRLNPEEAKACRRDGGQGVLSIESDEQKLEKFI 63
Db 1911 QEQCEGWTXFGQCYR--HFPD---RETWDAERCRQOQSHLSIVTPEQEFYNKNA 1965
Qy 64 ENLLPSDGF-WIGLRRREKQSNACQDLYAWTQSGISQFRNWVDEP-----SCGSEV 118
Db 1966 Q-----DYQWIGL-----NDRITGDFRWSGSHLSQFEKWRPNQDNFFATGDC 2010
Qy 119 CVVMYHQPSAPAGIGGYPWFQWNDRCNMKNFKYVS---DEKPAVPSRAEGETE 173
Db 2011 VVMINHERG-----EWNDFVCNQLPFTCKKGTACGPPAVEHARTLGQKD 2058

RESULT 19
PCGB BOVIN
ID PCGB BOVIN STANDARD; PRT; 912 AA.
AC Q28062;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Brevican core protein precursor.
GN BCAN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bevoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94193597; PubMed=8144512;
RA Yamada H., Watanabe K., Shimonaka M., Yamaguchi Y.;

FT	DISULFID	277	352	BY SIMILARITY.
FT	DISULFID	301	322	BY SIMILARITY.
FT	DISULFID	651	662	BY SIMILARITY.
FT	DISULFID	651	662	BY SIMILARITY.
FT	DISULFID	673	682	BY SIMILARITY.
FT	DISULFID	689	700	BY SIMILARITY.
FT	DISULFID	717	809	BY SIMILARITY.
FT	DISULFID	785	801	BY SIMILARITY.
FT	DISULFID	816	859	BY SIMILARITY.
FT	DISULFID	845	872	BY SIMILARITY.
FT	CARBOHYD	130	130	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	912 AA; 99554 NW; 677B3EB1C688C4D7	CRC64;	

Query Match 13.7%; Score 152; DB 1; Length 912;
 Best Local Similarity 28.6%; Pred.No. 8.7e-06;
 Matches 47; Conservative 17; Mismatches 61; Indels 38; Gaps 8;

QY	15	QRFCYKVIYFHDTSRLNPFEEAKEACRDGGOLVSIESDEQKLIEKFIENTLLPSDGDWF	74
DB	697	QGACYK-----HFSARR-SWEEAENKCRWYGAHLASISTPEEQDFINNRVREYQ-----W	745
QY	75	IGLRREKQSNSTACODIYAWTDGSIQFRWYVDERS---CGSEVCVM-YHQPSAFA	130
DB	746	IGL-----NDRITIEGDFLMSDGVPLLYENWNGQDPSYFLSGENCVMVWHDOG---	794
QY	131	GIGGPMFQWDRCKMKNFICKYS---DEKPAVPSREAEQ	169
DB	795	-----QWSDVPCNYHLSTYCKMGLVSCGPPPLPLAEVFG	829

RESULT 20
 CD93 HUMAN STANDARD; PRT; 652 AA.
 ID_CD93 HUMAN STANDARD; PRT; 652 AA.
 AC Q9N973; Q00274;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Complement component C1q receptor precursor (Complement component 1, q subcomponent, receptor 1) (C1qR(p) (C1qR(p)) (C1q/MBL/SPA receptor) (CD93 antigen) (CDw93).
 DE C1QRI OR CD93.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP MEDLINE=971199258; PubMed=9047234;
 RX Nephomuceno R.R., Henschen-Sdman A.H., Burgess W.H., Tenner A.J.;
 RX "cDNA cloning and primary structure analysis of C1qR(P), the human C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro.";
 RT Immunity 6:119-129(1997).
 RL [2]
 RP SEQUENCE FROM N.A., AND VARIANT ALA-318.
 RP MEDLINE=21640567; PubMed=11781389;
 RX Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,
 RX Prager E., Stafler G., Madic O., Stockinger H., Knapp W.;
 RA "Identification of human CD93 as the phagocytic C1q receptor (C1qRp) by expression cloning.";
 RL J. Leukoc. Biol. 71:133-140(2002).
 RL [3]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=21638749; PubMed=11780052;
 RX Delucas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguely C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn W.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

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CC Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., Mullikin J.C., McMurray A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20";
RL Nature 414:865-871 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Leukocyte;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=2190337; PubMed=11994479;
RA McGreal E.P., Ikegaki N., Akatsu H., Morgan B.P., Gasque P.;
RT "Human C1q is identical with CD93 and the mni-11 antigen but does
RT not bind C1q";
RL J. Immunol. 168:5222-5232 (2002).
RN [6]
RP O-GLYCOSYLATION.
RX MEDLINE=9919277; PubMed=10092817;
RA Neponuceno R.R., Ruiz S., Park M., Tenner A.J.;
RT "C1q is a heavily O-glycosylated cell surface protein involved in
RT the regulation of phagocytic activity";
RL J. Immunol. 162:3583-3589 (1999).
CC -!- FUNCTION: Receptor (or element of a larger receptor complex) for
CC C1q, mannose-binding lectin (MBL2) and pulmonary surfactant
CC protein A (SPA). May mediate the enhancement of phagocytosis in
CC monocytes and macrophages upon interaction with soluble defense
CC collagens. May play a role in intercellular adhesion.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in endothelial cells,
CC platelets, cells of myeloid origin, such as monocytes and
CC neutrophils. Not expressed in cells of lymphoid origin.
CC -!- PTM: N- and O-glycosylated.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 5 EGF-like domains.
CC -!- CAUTION: Has been sometimes referred to as a collectin receptor.
CC -!- CAUTION: According to Ref.5, C1q is not a ligand for C1QR1.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 3:1-6(2001);
CC WWW=http://www.ncbi.nlm.nih.gov/prov/guide/467246456_g.htm.
CC

EMBL; U94333; AAB53110.1; -;
EMBL; AL118508; CAC00597.1; -;
EMBL; BC028075; AAH28075.1; -;
HSP; P35555; IEMN.
Genew; HGNC:15955; C1QR1.
MIM; 120577;
GO; GO:0016021; C:integral to membrane; IC.
GO; GO:0004872; F:receptor activity; NAS.
GO; GO:0016337; P:cell-cell adhesion; IDA.
GO; GO:0042116; P:macrophage activation; NAS.
GO; GO:0006909; P:phagocytosis; NAS.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR001881; EGF_CA.
InterPro; IPR006209; EGF-like.
InterPro; IPR001304; Lectin_C.
Pfam; PF00008; EGF; 5.
Pfam; PF00059; LECTIN_C; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 3.
PROSITE; PS00010; ASX_HYDROXYL; 3. FALSE_NEG.
PROSITE; PS00615; C-TYPE LECTIN_1; 1.
PROSITE; PS00041; C-TYPE LECTIN_2; 1.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS00026; EGF_3; 3.
PROSITE; PS01187; EGF_CA; 3.
Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
EGF-like domain; Lectin; Glycoprotein; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 652
FT DOMAIN 24 580
FT TRANSMEM 581 601
FT DOMAIN 602 652
FT DOMAIN 32 174
FT DOMAIN 260 301
FT DOMAIN 302 344
FT DOMAIN 345 384
FT DOMAIN 385 426
FT DOMAIN 427 468
FT DOMAIN 594 601
FT DISULFID 264 275
FT DISULFID 271 285
FT DISULFID 287 300
FT DISULFID 306 317
FT DISULFID 311 328
FT DISULFID 330 343
FT DISULFID 349 358
FT DISULFID 354 367
FT DISULFID 369 383
FT DISULFID 389 400
FT DISULFID 396 409
FT DISULFID 411 425
FT DISULFID 431 443
FT DISULFID 439 452
FT DISULFID 454 467
FT CARBOHYD 325 325
FT VARIANT 318 318
FT CONFLICT 22 22
FT CONFLICT 36 36
FT CONFLICT 38 39
FT CONFLICT 155 155
FT CONFLICT 186 186
FT CONFLICT 492 492
FT CONFLICT 496 496
FT CONFLICT 504 504

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CC or send an email to license@isb-sib.ch).

FT CONFLICT 541 541 P -> S (IN REF. 1).
 SQ SEQUENCE 652 AA; 68560 MW; EECACFEAC5FCAC2 CRC64;
 Query Match 13.7%; Score 151.5; DB 1; Length 652;
 Best Local Similarity 24.4%; Pred. No. 6.4e-06;
 Matches 50; Conservative 38; Mismatches 74; Indels 43; Gaps 9;
 QY 3 LLSGQP-----VCRGTQPCYKVIYFHTSRRLNFEFAKEACRRDGGQGVLSIE 51
 Db 13 LLLTPGAGTGADTAVCVG---TACYTA-----HSGKLSAAEAQNHQNGNLTATVK 64
 QY 52 SRDEQKLEKFTENLLPSD-----GDFWIGURBREEKQNSTACQDLYAWT-DGSISQ 103
 Db 65 SKEEAHQVQVLAQLURREALTAARMSKEWIGLQREKGLDPSLPLKFSWVGGEPTP 124
 QY 104 FRNYYVD-EPSCGSEVYVM---YHQPAPAGIGGPGYFQWMDRCNMKN---FI 152
 Db 125 YSNWHELRNSCISKRCVSLLDLSQPLPLSLP-----KWSEGGPGSPGPNIEGFV 179
 QY 153 CKYSDEKPAVPSREAGESELTTP 177
 Db 180 CRFSFGMCRPLALGGPGQVYVTP 204

RESULT 21
 CLE1 HUMAN STANDARD; PRT; 197 AA.
 AC Q75596;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-type lectin superfamily member 1 precursor (Cartilage-derived C-type lectin).
 GN CLECSF1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cartilage;
 RX MEDLINE=99453719; PubMed=10524194;
 RA Neame P.J., Tapp H., Grimm D.R.;
 RT "The cartilage-derived, C-type lectin (CLECSF1): structure of the gene and chromosomal location."
 RL Biochim. Biophys. Acta 1446:193-202(1999).
 CC -!- TISSUE SPECIFICITY: Restricted to cartilage.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC -----
 DR EMBL; AF077345; AAD12542.1;
 DR EMBL; AF077344; AAD12542.1; JOINED.
 DR HSSP; P05452; 1HTN.
 DR Genew; HGNC:2052; CLECSF1.
 DR GO; GO:0005530; F:lectin; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin c. 1.
 DR SMART; SM00034; CLEC1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
 DR PROSITE; PS00441; C-TYPE LECTIN 2; 1.
 KW Lectin; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 197 C-TYPE LECTIN
 FT DOMAIN 74 192 C-TYPE LECTIN
 FT SUPERFAMILY MEMBER 1.

FT DISULFID 95 191 BY SIMILARITY.
 FT DISULFID 167 183 BY SIMILARITY.
 SQ SEQUENCE 197 AA; 22232 MW; BB924DBDB729A4 CRC64;
 Query Match 13.7%; Score 151; DB 1; Length 197;
 Best Local Similarity 25.08%; Pred. No. 1.6e-06;
 Matches 38; Conservative 26; Mismatches 64; Indels 24; Gaps 4;
 QY 7 QPVCRGQTQ--RPCYKVIYFHTSRRLNFEFAKEACRRDGGQGVLSIEDEQKLEKFTIE 64
 Db 65 QTVCLRTGKTVHKCYLA-----SEGLKHFHEANEDCISKGLIVIPRNSDEINALQDYGK 119
 QY 65 NLLPSDGDFFWIGURBREEKQNSTACQDLYAWT-DGSISQFRNYYVDPEPCGSEVYVMYH 124
 Db 120 RSLPGVNDFFWLG-----NDMVTEGKFDVYNGIAISFLNWDRAQPNKGKRENCVLS 171
 QY 125 QPSAPAGIGGPGYFQWMDRCNMKNFIKYS 156
 Db 172 QSA-----QGWSDACRSSKEYICEPT 194
 RESULT 22
 FCE2 HUMAN STANDARD; PRT; 321 AA.
 ID FCE2 HUMAN
 AC P06734;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Low affinity immunoglobulin epsilon FC receptor (Lymphocyte IgE receptor) (FC-epsilon-RII) (CD23) (BLAST-2) (Immunoglobulin E-binding factor).
 DE FCER2 OR IGBEF.
 GN FCER2 OR IGBEF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87118255; PubMed=2949326;
 RA Ikuta K., Takami M., Kim C.W., Honjo T., Miyoshi T., Tagaya Y., Kawabe T., Iodoi J.;
 RT "Human lymphocyte Fc receptor for IgE: sequence homology of its cloned cDNA with animal lectins."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87051737; PubMed=2877743;
 RA Kikutani H., Inui S., Sato R., Barsumian E.L., Owaki H., Yamaeaki K., Kaisho T., Uchibayashi N., Hardy R.R., Hirano T., Tsunasawa S., Sakiyama F., Suemura M., Kishimoto T.;
 RT "Molecular structure of human lymphocyte receptor for immunoglobulin E."
 RL Cell 47:657-665(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87218454; PubMed=3034567;
 RA Luedin C., Hofstetter H., Sarfati M., Levy C.A., Suter U., Alaimo D., Kilchherr E., Frost H., Delespesse G.;
 RT "Cloning and expression of the cDNA coding for a human lymphocyte IgE receptor."
 RL EMBO J. 6:109-114(1987).
 RN [4]
 RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=93038513; PubMed=1417742;
 RA Rose K., Turcatti G., Graber P., Pochon S., Regamey P.-O., Jansen K.U., Magnenat E., Aubonne N., Bonnefoy J.-Y.;
 RT "Partial characterization of natural and recombinant human soluble CD23."
 RL Biochem. J. 286:819-824(1992).
 RN [5]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=89028672; PubMed=2972386;

RA Suemura M., Kishimoto T.;
RT "Two species of human Fc epsilon receptor II (Fc epsilon RII/CD23):
RI tissue-specific and IL-4-specific regulation of gene expression.";
RL Cell 55:611-618(1988).
RW [6]
RX 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
RY MEDLINE=94191542; PubMed=8142907;
RA Padlan E.A., Helm B.A.;
RT "Modeling of the lectin-homology domains of the human and murine low-
RI affinity Fc epsilon receptor (Fc epsilon RII/CD23).";
RL Receptor 3:325-341(1993).
RW [7]
RX 3D-STRUCTURE MODELING OF 173-285.
RY MEDLINE=96276216; PubMed=8745401;
RA Bajorath J., Aruffo A.;
RT "Structure-based modeling of the ligand binding domain of the human
RI cell surface receptor CD23 and comparison of two independently
RL derived molecular models";
RL Protein Sci. 5:240-247(1996).
CC -!- FUNCTION: This receptor has essential roles in the regulation of
CC IgE production and in the differentiation of B-cells (it is a B-
CC cell-specific antigen).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS A
CC SOLUBLE EXCRETED FORM.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P06734-1; Sequence=D66734; Sequence=VSP_003057;
CC Name=B;
CC IsoId=P06734-2; Sequence=VSP_003057;
CC -!- PTM: N- and O-glycosylated.
CC -!- MISCELLANEOUS: There are two kinds of Fc receptors for IgE, which
CC differ in both structure and function: high affinity receptors on
CC basophils and mast cells and low affinity receptors on lymphocytes
CC and monocytes.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD23 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd23.htm".
CC
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CC
CC EMBL; M15059; AA52434.1; -;
CC EMBL; M14765; AA52435.1; -;
CC EMBL; X04772; CAA28465.1; -;
CC EMBL; M23562; AA52433.1; -;
CC PIR; A26067; LNHUER.
CC PDB; 1HLI; 31-JAN-94.
CC PDB; 1KJE; 03-APR-96.
CC Genew; HGNC:3612; FCER2.
CC
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005178; F:integrin binding; TAS.
CC InterPro; IPR02353; AntifreezeII.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; Lectin_C; 1.
CC PRINTS; PR00356; ANTIIFREEZEII.
CC SMART; SM00034; CLEET; 1.
CC PROSITE; PS00615; C-TYPE LECTIN 1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Receptor; Antigen; IgE-binding protein; Repeat; Signal-anchor;
KW Transmembrane; Lectin; Glycoprotein; Alternative splicing;
KW 3D-structure.
FT CHAIN 1 321 MEMBRANE BOUND FORM.
FT CHAIN 150 321 SOLUBLE FORM.
FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 22 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).

FT DOMAIN 48 321 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 162 284 C-TYPE LECTIN (LONG FORM).
FT SITE 149 150 CLEAVAGE.
FT REPEAT 69 89
FT REPEAT 90 110
FT REPEAT 111 131
FT REPEAT 160 288 BY SIMILARITY.
FT DISULFID 163 174 BY SIMILARITY.
FT DISULFID 191 282
FT DISULFID 259 273
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 1 7 MEEGOYS -> MNPPSQ (in isoform B).
FT CONFLICT 269 269 /FTId=VSP_003057.
FT STRAND 174 177 N -> T (IN REF. 3).
FT HELIX 184 193
FT TURN 194 195
FT STRAND 197 198
FT HELIX 204 214
FT TURN 215 216
FT STRAND 219 228
FT TURN 229 230
FT STRAND 231 234
FT TURN 235 236
FT STRAND 239 239
FT TURN 245 245
FT TURN 247 248
FT STRAND 254 255
FT TURN 259 262
FT STRAND 264 265
FT TURN 268 271
FT TURN 273 274
FT STRAND 281 284
SQ SEQUENCE 321 AA; 36468 MW; F86708C0E515B87 CRC64;
Query Match 13.5%; Score 149; DB 1; Length 321;
Best Local Similarity 30.2%; Pred. NO. 4.5e-06;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;
QY 15 ORPCYKVIYFHTSRRLNFEBAKRCRDGGQGVLSIEDSEQKLEKIENLLPSDGF 74
DB 171 ORKCY---YFGKTKQ--WVHARYACDDMEGOLVSHSPEDQFLTKH-----ASHTGSW 220
QY 75 IGLRREKQSNSTACQDLYAMTDGSIQFRWYVDPEFCGS--EVCVVMYHQPAPAGI 132
DB 221 IGLRLDLKGE-----FIWVDSGVHDYSNWPGEPTSRSGQSDCVMM-----RGS 265
QY 133 GGPYMFQWDDRCNMK--NNFICKYSDKPAV---PSREAGE-----ETELTTPV 178
DB 266 G-----RWNDAFCDRLKGAWC-----DRLATCTPPASGSASMGPSRDPDGLPTPS 316
QY 179 LP 180
DB 317 AP 318
RESULT 23
PGCA MOUSE
ID PGCA MOUSE STANDARD; PRT; 2132 AA.
AC Q61282; Q64021;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggregran core protein precursor (Cartilage-specific proteoglycan core
DE protein) (GSPCP).
GN AGC1 OR AGC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Cartilage;

RX MEDLINE=95104847; PubMed=7806222;
 RA Walcz E., Deak F., Erhardt P., Coulter S.N., Fuellep C., Horvath P.,
 RA Doege K.J., Glant T.T.;
 RT "Complete coding sequence, deduced primary structure, chromosomal
 RT localization, and structural analysis of murine aggrecan.";
 RL Genomics 22:364-371(1994).
 RN [2]
 RP SEQUENCE OF 211-326 FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=95004579; PubMed=7920633;
 RA Watanabe H., Kimata K., Line S., Strong D., Gao L.-Y., Kozak C.A.,
 RA Yamada Y.;
 RT "Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in
 RT the aggrecan gene";
 RL Nat. Genet. 7:154-157(1994).
 RN [3]
 RP INTERACTION WITH FBLN1.
 RX MEDLINE=99329059; PubMed=10400671;
 RA Asperberg A., Adam S., Kostka G., Timpl R., Heinigaard D.;
 RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
 RT versican.";
 RL J. Biol. Chem. 274:20444-20449(1999).
 CC -!- FUNCTION: This proteoglycan is a major component of extracellular
 CC matrix of cartilaginous tissues. A major function of this protein
 CC is to resist compression in cartilage. It binds avidly to
 CC hyaluronic acid via an amino-terminal globular region. May play a
 CC regulatory role in the matrix assembly of the cartilage.
 CC -!- SUBUNIT: Interacts with FBLN1.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
 CC terminus of the proteoglycan, while another globular region, G3,
 CC makes up the COOH terminus. G1 contains link domains and thus
 CC consists of three disulfide-bonded loop structures designated as
 CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
 CC and the chondroitin sulfate (CS) attachment domains lie between G2
 CC and G3.
 CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
 CC chains, N-linked and O-linked oligosaccharides.
 CC -!- DISBASE: Defects in AGC1 are the cause of cartilage matrix
 CC deficiency (CMD). CMD is an autosomal recessive syndrome
 CC characterized by cleft palate, short limbs, tail and snout.
 CC Mutation in strain CMD causes absence of aggrecan by truncation of
 CC the protein (mutation in the G1 domain).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 4 link domains.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
 CC
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 CC -----
 CC EMBL: L07049; AAC37670.1; -;
 CC EMBL: S73722; AAB32160.1; -;
 CC EMBL: S73721; AAB32160.1; JOINED.
 CC PIR: A55182; A55182.
 CC HSP: P98066; 17SG.
 CC MGI: 99602; Agcl.
 CC InterPro: IPR002353; AntifreezeII.
 CC InterPro: IPR007110; IG-like.
 CC InterPro: IPR003006; IG_MHC.
 CC InterPro: IPR003596; IG_V.
 CC InterPro: IPR001304; Lectin_C.
 CC InterPro: IPR000538; Link.
 CC InterPro: IPR003324; SGXSG.
 CC InterPro: IPR000436; Sushi_SCR_CCP.

DR Pfam: PF00047; ig; 1.
 DR Pfam: PF00059; lectin_c; 1.
 DR Pfam: PF02339; SGXSG; 60.
 DR Pfam: PF00084; sushi; 1.
 DR Pfam: PF00193; Xlink; 4.
 DR PRINTS: PR00356; ANTIFREEZEII.
 DR PRINTS: PR01265; LINKMODULE.
 DR PRODOM: PD000918; Link; 4.
 DR SMART: SMC0032; CCP; 1.
 DR SMART: SMC0034; CLECT; 1.
 DR SMART: SMC0406; IG; 1.
 DR SMART: SMC0445; LINK; 4.
 DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE: PS00041; C-TYPE LECTIN_2; 1.
 DR PROSITE: PS00835; IG LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PROSITE: PS01241; LINK; 4.
 DR Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; Repeat;
 KW Immunoglobulin domain.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 2132 AGGREGAN CORE PROTEIN.
 FT DOMAIN 34 147 IG-LIKE V-TYPE.
 FT DOMAIN 170 247 LINK 1.
 FT DOMAIN 268 349 LINK 2.
 FT DOMAIN 504 581 LINK 3.
 FT DOMAIN 602 683 LINK 4.
 FT DOMAIN 1918 2044 C-TYPE LECTIN.
 FT DOMAIN 2048 2106 SUSHI.
 FT DOMAIN 48 140 G1-A.
 FT DOMAIN 152 247 G1-B.
 FT DOMAIN 253 349 G1-B'.
 FT DOMAIN 486 580 G2-B.
 FT DOMAIN 587 682 G2-B'.
 FT DOMAIN 685 803 KS.
 FT DOMAIN 805 1231 CS-1.
 FT DOMAIN 1232 1917 CS-2.
 FT DOMAIN 1917 2132 G3.
 FT DISULFID 51 133 BY SIMILARITY.
 FT DISULFID 175 246 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT DISULFID 273 348 BY SIMILARITY.
 FT DISULFID 297 318 BY SIMILARITY.
 FT DISULFID 509 580 BY SIMILARITY.
 FT DISULFID 533 554 BY SIMILARITY.
 FT DISULFID 607 682 BY SIMILARITY.
 FT DISULFID 631 652 BY SIMILARITY.
 FT DISULFID 1922 1933 BY SIMILARITY.
 FT DISULFID 1950 2042 BY SIMILARITY.
 FT DISULFID 2018 2034 BY SIMILARITY.
 FT DISULFID 2049 2092 BY SIMILARITY.
 FT DISULFID 2078 2105 BY SIMILARITY.
 FT CARBOHYD 126 165 N-LINKED (GLCNAC...)
 FT CARBOHYD 239 239 N-LINKED (GLCNAC...)
 FT CARBOHYD 333 333 N-LINKED (GLCNAC...)
 FT CARBOHYD 387 387 N-LINKED (GLCNAC...)
 FT CARBOHYD 611 611 N-LINKED (GLCNAC...)
 FT CARBOHYD 667 667 N-LINKED (GLCNAC...)
 FT CARBOHYD 1675 1675 N-LINKED (GLCNAC...)
 FT SITE 1171 1173 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 2132 AA; 222008 MW; 0B2BCDFC6CDA163 CRC64;
 Query Match 13.3%; Score 147.5; DB 1; Length 2132;
 Best Local Similarity 24.7%; Pred. No. 6.3e-05;
 Matches 45; Conservative 30; Mismatches 64; Indels 43; Gaps 9;
 QY 4 LSCQVPCRGG---TORPCYKVIYFHDTSRRNFPEAKEACRRDGGQLVSISEDEBQKLE 60
 Db 1916 VADQFCCEGWTKFGHCYR--HFPD---RETWDAERCRCEQQSHLSIVTFEEQFVN 1970
 QY 61 KFIENLLFSDGDF-WIGLRRREKQSNSTACQDLYAMTDGSIQFRNYYVDEP-----SCG 115
 Db 1971 KNAQ-----DYOWIGL-----NDRITTEGDFRMSDGHSLQFEKWRPNQPNFFATG 2015

FT	DOMAIN	1855	1892	EGF-LIKE.
FT	DOMAIN	1901	2019	C-TYPE LECTIN.
FT	DOMAIN	2023	2081	SUSHI.
FT	DOMAIN	48	137	G1-A.
FT	DOMAIN	148	243	G1-B.
FT	DOMAIN	249	346	G1-B'.
FT	DOMAIN	519	613	G2-B.
FT	DOMAIN	620	715	G2-B'.
FT	DOMAIN	718	803	KS.
FT	DOMAIN	805	1264	CS-1.
FT	DOMAIN	1265	1742	CS-2.
FT	DOMAIN	1893	2109	G3.
FT	DISULFID	51	129	BY SIMILARITY.
FT	DISULFID	171	242	BY SIMILARITY.
FT	DISULFID	195	216	BY SIMILARITY.
FT	DISULFID	269	345	BY SIMILARITY.
FT	DISULFID	293	314	BY SIMILARITY.
FT	DISULFID	542	613	BY SIMILARITY.
FT	DISULFID	566	587	BY SIMILARITY.
FT	DISULFID	640	715	BY SIMILARITY.
FT	DISULFID	664	685	BY SIMILARITY.
FT	DISULFID	1859	1870	BY SIMILARITY.
FT	DISULFID	1864	1879	BY SIMILARITY.
FT	DISULFID	1881	1890	BY SIMILARITY.
FT	DISULFID	1897	1908	BY SIMILARITY.
FT	DISULFID	1925	2017	BY SIMILARITY.
FT	DISULFID	1993	2009	BY SIMILARITY.
FT	DISULFID	2024	2067	BY SIMILARITY.
FT	DISULFID	2053	2080	BY SIMILARITY.
FT	CARBOHYD	76	76	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	122	122	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	388	388	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	644	644	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	700	700	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	765	765	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	801	801	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPIC	1856	1892	Missing (in isoform 2).
FT	CONFLICT	362	362	/FTid=VSP 003073.
FT				E -> D (IN REF. 3).

Query Match 13.2%; Score 146; DB 1; Length 2109;
Best Local Similarity 25.0%; Pred. No. 8.5e-05;
Matches 42; Conservative 28; Mismatches 58; Indels 40; Gaps 8;

QY	15	ORPCYKVIYFDTSRLNFEAKACRRDGGQLVSEDEQKLIKFIENLLPSDGF-73
Db	1905	QCHCYR--HFEZ---RETWDAESCREHQHLSIIITPEQBFVNSHAQ-----DYQ 1952
QY	74	WIGLRREEKOSNSTACQDLVATDGSISQFRNWTVDPS-----CGSEVCVVMYHQSAP 129
Db	1953	WIGLSDR-----AVENDFRWSDGHSLOFENWRFPQDNFFPAGEDCVVMWHEQG-- 2002
QY	130	AGIGGPYVFQNDRCNNKNFICKYS---DEKPAVPSREAGEBETE 173
Db	2003	-----EWDVPCNHLPTCKKGVACGDPVVENATFRKKD 2041

Search completed: September 9, 2004, 22:54:11
Job time : 16.0369 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:47:24 ; Search time 72.1769 Seconds
(without alignments)
891.777 Million cell updates/sec

Title: US-09-887-855-2_COPY_24_227

Perfect score: 1106

Sequence: 1 GRLLSGQPVCRGGTQRPCYK.....EEDAKTFFKSRREALNLAY 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archheap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1106	100.0	374	Q8TAY8	Q8tay8 homo sapien
2	1106	100.0	374	Q96NF3	Q96nf3 homo sapien
3	1102	99.6	374	Q96NC5	Q96nc5 homo sapien
4	945.5	85.5	374	Q9Z209	Q9z209 cricetulus
5	803.5	72.6	211	Q8C351	Q8c351 mus musculus
6	580	52.4	246	Q8BM17	Q8bm17 mus musculus
7	580	52.4	292	Q8BVU2	Q8bvu2 mus musculus
8	513	46.4	236	Q7Z798	Q7z798 homo sapien
9	504.5	45.6	232	Q7Z799	Q7z799 homo sapien
10	500	45.2	236	Q7Z7A0	Q7z7a0 homo sapien
11	185	16.7	1290	Q9W6E1	Q9w6e1 gallus gall
12	178.5	16.1	1456	Q61830	Q61830 mus musculus
13	177.5	16.0	1348	Q25199	Q25199 hydra atten
14	176.5	16.0	1479	Q9Y5P9	Q9y5p9 homo sapien
15	176.5	16.0	1479	Q9UBG0	Q9ubg0 homo sapien
16	170.5	15.4	1479	Q64449	Q64449 mus musculus

17	169	15.3	217	11	Q8C4F8	Q8c4f8 mus musculus
18	165.5	15.0	742	11	Q8K4Q8	Q8k4q8 mus musculus
19	165.5	15.0	742	11	Q8C979	Q8c979 mus musculus
20	161.5	14.6	134	5	Q9XXY3	Q9xyx3 hydra magni
21	159.5	14.4	742	11	Q8VIF6	Q8vif6 mus musculus
22	158	14.3	142	11	Q8CJ86	Q8cj86 mus musculus
23	158	14.3	142	11	Q8BHK7	Q8bhk7 mus musculus
24	158	14.3	295	11	Q91ZM4	Q91zm4 mus musculus
25	158	14.3	311	11	Q9D8V4	Q9d8v4 mus musculus
26	158	14.3	325	11	Q91ZX0	Q91zx0 mus musculus
27	157	14.2	158	13	Q90WI7	Q90wi7 bungarus fa
28	156	14.1	323	11	Q8CJ91	Q8cj91 mus musculus
29	156	14.1	339	6	Q95244	Q95244 sus scrofa
30	155	14.0	293	11	Q8BGZ0	Q8bgz0 mus musculus
31	155	14.0	293	11	Q8CJ94	Q8cj94 mus musculus
32	155	14.0	323	11	Q8CJ93	Q8cj93 mus musculus
33	155	14.0	323	11	Q8CJ88	Q8cj88 mus musculus
34	155	14.0	379	11	Q7TMA7	Q7tma7 mus musculus
35	155	14.0	473	11	Q7TSP9	Q7tsp9 mus musculus
36	155	14.0	477	11	Q7TSQ7	Q7tsq7 mus musculus
37	155	14.0	504	11	Q7TSQ0	Q7tsq0 mus musculus
38	155	14.0	534	11	Q7TSQ1	Q7tsq1 mus musculus
39	155	14.0	1152	13	Q90WM2	Q90wm2 xenopus lae
40	154	13.9	322	11	Q8CJ89	Q8cj89 mus musculus
41	154	13.9	323	11	Q8CJ92	Q8cj92 mus musculus
42	153	13.8	446	4	Q725K9	Q725k9 homo sapien
43	152.5	13.8	485	6	Q95LQ3	Q95lq3 odocoileus
44	152	13.7	158	13	Q90WI6	Q90wi6 bungarus mu
45	151.5	13.7	652	4	Q81XK1	Q81xk1 homo sapien

ALIGNMENTS

RESULT 1

Q8TAY8

ID Q8TAY8 PRELIMINARY; PRT; 374 AA.

AC Q8TAY8; 2002 (Tremblrel. 21, Created)

DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Similar to unnamed protein product.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Strausberg R.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC025407; A825407.1; -

DR GO; GO:0005529; F:sugar binding; IEA.

DR InterPro; IPR001304; Lectin_C.

DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00041; C TYPE LECTIN 2; 1.

SQ SEQUENCE 374 AA; -42312 MW; FC214E6BC9E578D9 CRC64;

Query Match 100.0%; Score 1106; DB 4; Length 374;

Best local similarity 100.0%; Pred. No. 4.6e-98;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRLLSGQPVCRGGTQRPCYKVIYFHDTSRLNFEFAKEACRRDGGQGVLSIESDEQKLE 60

Db 24 GRLLSGQPVCRGGTQRPCYKVIYFHDTSRLNFEFAKEACRRDGGQGVLSIESDEQKLE 83

Qy 61 KFIENLLPSDGFWMGLRRREEKQSNSTACQDIYAWTDGSIQFRNRYVDEPSCGSEVCV 120

Db 84 KFIENLLPSDGFWMGLRRREEKQSNSTACQDIYAWTDGSIQFRNRYVDEPSCGSEVCV 143

Qy 121 VMYHQSAPAGICGPPYFQWMDRCNMKNFICKYSDKEPAVPSRAEGEETLTPVLP 180


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QY 1 GRLLSGQVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLE 60
DB 24 GRLLSGQLVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLE 83
QY 61 KFIEINLPSDGFDFWIGLRREKQSNSTACODLYAWTDGSIQFRNRYVDEPSPGSEVCV 120
DB 84 KFIEINLLASDGFDFWIGLRLEVKQVNTACODLYAWTDGSIQFRNRYVDEPSPGSEVCV 143
QY 121 VMYHQPSAPAGIGGPFYQWMDRCNMKNFNICKYDEKPA-VPSREABGEETELTPVL 179
DB 144 VMYHQPSAPAGIGGPFYQWMDRCNMKNFNICKYDEKPA-VPSREABGEETELTPVL 203
QY 180 PEETQEDAKTKTFKESREAAANLAY 204
DB 204 PEETQEDAKTKTFKESREAAANLAY 228

RESULT 5
ID Q8C351 PRELIMINARY; PRT; 211 AA.
AC Q8C351,
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE LAYILIN homolog (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK086930; BAC39765.1; -.
DR MGD; MGI:2179069; Chodl.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
FT NON_TER 211
SQ SEQUENCE 211 AA; 23697 MW; AD9870B5957DD5AE CRC64;

Query Match 72.6%; Score 803.5; DB 11; Length 211;
Best Local Similarity 79.8%; Pred. No. 3e-59;
Matches 150; Conservative 9; Mismatches 20; Indels 9; Gaps 2;

QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSI 52
DB 24 GRLLSASLDLPRGGLVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSI 83
QY 53 EDEQKLEKFTENLLPSDGFDFWIGLRREKQSNSTACODLYAWTDGSIQFRNRYVDEP 112
DB 84 EDEQKLEKFTENLLASDGFDFWIGLRLEKQSNSTACODLYAWTDGSIQFRNRYVDEP 143
QY 113 SCGSEVCVMYHQPSAPAGIGGPFYQWMDRCNMKNFNICKYDEKPA-VPSREABGE 171
DB 144 SCGSEVCVMYHQPSAPAGIGGPFYQWMDRCNMKNFNICKYDEKPA-VPSREABGE 203
QY 172 TELTTPVL 179
DB 204 TEPATPLL 211

RESULT 6
Q8BM17 PRELIMINARY; PRT; 245 AA.
ID Q8BM17
AC Q8BM17,

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DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE C-type lectin protein MT75 homolog.
GN CHODL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK031063; BAC27234.1; -.
DR MGD; MGI:2179069; Chodl.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 246 AA; 27394 MW; E872660C58267752 CRC64;

Query Match 52.4%; Score 580; DB 11; Length 246;
Best Local Similarity 57.9%; Pred. No. 1.1e-47;
Matches 110; Conservative 26; Mismatches 40; Indels 14; Gaps 5;

QY 2 RLSSGQVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLEK 61
DB 23 RVVSGQKVCFADVKHPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLEK 82
QY 62 FIENLLP-----SDGDFWIGLRREKQSNSTACODLYAWTDGSIQFRNRYVDEPSCGS 116
DB 83 MLCNLTGKPTGSDGDFWIGLRREKQSNSTACODLYAWTDGSIQFRNRYVDEPSCGS 141
QY 117 EVCVMYHQPSAPAGIGGPFYQWMDRCNMKNFNICKYDEKPA-VPSREABGEETELT 175
DB 142 EKCVMYHQPTANPLGGLVYQWMDRCNMKNFNICKYDEKPA-VPSREABGEETELT 196
QY 176 TPVLPPEQTQ 185
DB 197 NQ--PEETHE 204

RESULT 7
Q8BVU2 PRELIMINARY; PRT; 292 AA.
ID Q8BVU2
AC Q8BVU2,
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE C-type lectin protein MT75 homolog.
GN CHODL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK076523; BAC36378.1; -.
DR MGD; MGI:2179069; Chodl.
DR GO; GO:0005529; F:sugar binding; IEA.

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[illegible]

131 GIGGPFQWDDRCNNKNNFICK 154
 1160 -IG-----KWNDVPCNNLPYICK 1177

QY
 Db

RESULT 12
 Q61830
 ID Q61830 PRELIMINARY; PRT; 1456 AA.
 AC Q61830;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Macrophage mannose receptor precursor.
 GN MRC1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=100390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=93043353; PubMed=1421407;
 RA Harris N., Rits M., Chang G., Ezekowitz R.B.;
 RT "Characterization of the murine macrophage mannose receptor."
 RL Blood 80:2363-2373(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Super M.;
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z11974; CAA78028.1;
 DR PIR: A48225; A48925.
 DR PDB: 1DQG; 10-MAY-00.
 DR PDB: 1DQO; 10-MAY-00.
 DR PDB: 1FWU; 17-JAN-01.
 DR PDB: 1FWV; 17-JAN-01.
 DR MGD: MGI:97142; Mrc1.
 DR GO: GO:0009928; C:cell surface (sensu Magnoliophyta); IDA.
 DR GO: GO:0005337; F:mannose binding; IDA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IDA.
 DR InterPro: IPR002383; AntifreezeII.
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR008997; RicinB-like.
 DR InterPro: IPR000772; Ricin_E_lectin.
 DR Pfam: PF00040; fn2; 1.
 DR Pfam: PF00059; lectin_c; 8.
 DR Pfam: PF00652; Ricin_E_lectin; 2.
 DR PRINTS: PR00356; ANTIFREEZEII.
 DR PRINTS: PR00013; FNTYPEII.
 DR ProDom: PD000995; FN_Type_II; 1.
 DR SMART: SM00034; CLECT; 8.
 DR SMART: SM00059; FN2; 1.
 DR SMART: SM00458; RICIN; 1.
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 6.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 8.
 DR PROSITE: PS00023; FIBRONECTIN_2; 1.
 DR PROSITE: PS50231; RICIN_B_LLECTIN; 1.
 KW Receptor; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 1456 MACROPHAGE MANNOSE RECEPTOR.
 SQ SEQUENCE 1456 AA; 165065 MW; 4EBD3F1B8619A594 CRC64;

Query Match 16.1%; Score 178.5; DB 11; Length 1456;
 Best Local Similarity 25.9%; Pred. No. 4.2e-08;
 Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;

QY 19 YKVIYFHTSRRUNFBEAKACRRDGGQLVSISEDEQKLEKFIENLLPSDGDFFWIGLR 78
 807 YKDYQYFSEKEMTDNARRFCKNFGLATIKSESEKFLWKYI-NKNGQSPYFIGML 865

QY 79 RREKQSNSTACQDLAWTDGSIQFRNMYVDPSGCS--EVCVAVHQPASAGIGPY 136

151 GIGGPFQWDDRCNNKNNFICK 154
 1160 -IG-----KWNDVPCNNLPYICK 1177

QY
 Db

RESULT 11
 Q9W6E1
 ID Q9W6E1 PRELIMINARY; PRT; 1290 AA.
 AC Q9W6E1;
 DT 01-NOV-1999 (TREMELrel. 12, Created)
 DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Neurocan core protein.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20309833; PubMed=10851024;
 RA Li H., Leung T.C., Hoffman S., Balsamo J., Lilien J.;
 RT "Coordinate Regulation of Cadherin and Integrin Function by the
 Chondroitin Sulfate Proteoglycan Neurocan."
 RL J. Cell Biol. 149:1275-1288(2000).
 DR EMBL: AF116856; AAD24546.2; -.
 DR HSSP: P08709; 1BF9.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0005540; F:hyaluronic acid binding; IEA.
 DR GO: GO:0005529; F:sugar binding; IEA.
 DR GO: GO:0007155; F:cell adhesion; IEA.
 DR InterPro: IPR00152; Asx hydroxyl_S.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR000538; Link.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00047; IG; 1.
 DR Pfam: PF00059; lectin_c; 1.
 DR Pfam: PF00084; sushi; 1.
 DR Pfam: PF00193; Xlink; 2.
 DR PRINTS: PR00010; EGFELOOD.
 DR PRINTS: PR01265; LINKMODULE.
 DR ProDom: PD000918; Link; 2.
 DR SMART: SM00032; CCP; 1.
 DR SMART: SM00034; CLECT; 1.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00445; LINK; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 DR PROSITE: PS00022; EGF_1; 2.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR PROSITE: PS01241; LINK; 2.
 KW EGF-like domain.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 1456 MACROPHAGE MANNOSE RECEPTOR.
 SQ SEQUENCE 1290 AA; 138877 MW; 182BD86D0E40BE78 CRC64;

Query Match 16.7%; Score 185; DB 13; Length 1290;
 Best Local Similarity 34.7%; Pred. No. 8.6e-09;
 Matches 50; Conservative 18; Mismatches 42; Indels 34; Gaps 8;

QY 15 QPFCVKYVHTSRLNFEAKACRRDGGQLVSISEDEQKLEKFIENLLPSDGDFFW 74
 1064 QGHCYR--YF---SRRSWEDAERDCRRRAGHLTSIHQSEPHGFINSF-----GHENTW 1112

QY 75 IGLRREKQSNSTACQDLAWTDGSIQFRNMYVDPSGCS--CGSEVCVVMY-HQPSAPA 130
 1113 IGLNDRIVEQD-----FQWTDNTGLQYENWRENQPDNPFAGGDCVILVSHE----- 1159

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Db 866 ISMDKK-----FIWDSKVDFAVATGEPNFANDENCVTMY-----TNSGF----- 908
QY 137 MFQWDDRCNMKNFICK--YSDEKPAVPSREAGEETELTTPVLPETQF----- 185
Db 909 ---WINDGCVYNNFICRHHSSINATAMP-----TTPTPGGCKEGHLYKNK 954
QY 186 -----EDAKTKFESREALNL 202
Db 955 CFKIFGFANEKKSQDARQACKGL 979
RESULT 13
Q25199 PRELIMINARY; PRT; 1348 AA.
AC Q25199;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tyrosine kinase receptor.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Irvine;
RC MEDLINE=20209407; PubMed=10744720;
RA Reidling J.C., Miller M.A., Steele R.E.;
RT "Sweet Tooth, a Novel Receptor Protein-tyrosine Kinase with C-type
Lecsin-like Extracellular Domains";
RL J. Biol. Chem. 275:10323-10330(2000).
DR EMBL; J22612; AAA29218.2; -.
DR HSP; F11362; 1FCX.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR003990; Pancreatins ac.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00059; lectin_c; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot Kinase; 2.
DR SMART; SM00034; CLECT; 4.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 2.
DR PROSITE; PS00441; C TYPE LECTIN 2; 4.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
QY 4 LSGQFVC--RGGTQPC-----YKVIYFHTSRRLNFEFAKEACRRDGGQLVSISEDE 55
Db 412 LSHRFICKVRATNEYCAEGTSYRIYCFYISIFDFKFSQCNIGNLLIENQEE 471
QY 56 QKLEKFTENLPDGD--FWIGLR-----REEKQSNSTACQDLYAMTDSISQFRNRY 108
Db 472 ----NRFIENDLIKNDKYWIKNINWYDLKKNR-----FEWSDNTYTFQFNWI 518
QY 109 VDEP--SGSEVVCVVMYHQPAPAGIGGPFYQWNDRCNMKNFICK 154
Db 519 TNQPNNGIBSCVENYN-----GWSDECKVNLGPFICK 553

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RESULT 14
Q9Y5P9 PRELIMINARY; PRT; 1479 AA.
AC Q9Y5P9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Endocytic receptor Endo180.
GN ENDO180.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20148849; PubMed=10583150;
RA Sheikh H., Farwood H., Ashworth A., Isaack C.;
RT "Endo180, an endocytic recycling glycoprotein related to the
macrophage mannose receptor is expressed on fibroblasts, endothelial
RT cells and macrophages and functions as a lectin receptor.";
RL J. Cell Sci. 113:1021-1032(2000).
DR EMBL; AF134838; AAD30280.1; -.
DR HSP; P02751; 2FN2.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000562; FN Type II.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR000586; Lipoclin_cytFABP.
DR InterPro; IPR008997; RicinB_Like.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c; 8.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN Type II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 3.
DR PROSITE; PS00441; C TYPE LECTIN 2; 8.
DR PROSITE; PS00023; FIBONECTIN 2; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS00231; RICIN_B_LECTIN; 1.
DR Receptor.
QY 5 SGQVCRGGTQPCYKVIYFHTSRRLNFEFAKEACRRDGGQLVSISEDEOKLIEKTE 64
Db 385 SWQPF-----QGHCVRL-----QAEKRSWQESKKACLRGGDLVSIHMAELEFITKQIK 434
QY 65 NLLPSDGFWIGLRREEKQSNSTACQDLYAMTDSISQFRNRYVDEPS---CGSEVCV 121
Db 435 QEVE---ELWIGL-----NDLKLQNMFEWSDGLSVFTHHFPFNNFRDSDLCVT 483
QY 122 MYHQPAPAGIGGPFYQWNDRCNMKNFICKYDEKPAVPSRAEG 169
Db 484 IW---GPEG-----RWNDSPCNQSLPSICKKAGQLSQGAEEHDHG 520
Query Match 16.0%; Score 176.5; DB 4; Length 1479;
Best Local Similarity 30.4%; Pred. No. 6.7e-08;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;
QY 5 SGQVCRGGTQPCYKVIYFHTSRRLNFEFAKEACRRDGGQLVSISEDEOKLIEKTE 64
Db 385 SWQPF-----QGHCVRL-----QAEKRSWQESKKACLRGGDLVSIHMAELEFITKQIK 434
QY 65 NLLPSDGFWIGLRREEKQSNSTACQDLYAMTDSISQFRNRYVDEPS---CGSEVCV 121
Db 435 QEVE---ELWIGL-----NDLKLQNMFEWSDGLSVFTHHFPFNNFRDSDLCVT 483
QY 122 MYHQPAPAGIGGPFYQWNDRCNMKNFICKYDEKPAVPSRAEG 169
Db 484 IW---GPEG-----RWNDSPCNQSLPSICKKAGQLSQGAEEHDHG 520
RESULT 15
Q9UEGO PRELIMINARY; PRT; 1479 AA.
AC Q9UEGO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

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DR Urokinase receptor-associated protein UPARAP.
GN KIAA0709
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Behrendt N., Jensen O.N., Engelholm L.H., Mortz E., Mann M., Dano K.;
RT "A urokinase receptor-associated protein with specific collagen-
binding properties.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
EX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
DR EMBL; AF107292; AAF14192.1; -;
DR EMBL; AB014609; BAA1684.1; -;
DR HSP; P02751; 2FN2.
DR Genew; HGNC:16875; MRC2.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005215; P:electron transport; IEA.
DR GO; GO:0006110; P:transport; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR008997; RicinB_Like.
DR InterPro; IPR000772; Ricin_E_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; fn2; 1.
DR PRINTS; PR00059; lectin_c; 8.
DR PRINTS; PR000356; ANTIFREEZEII.
DR PRINTS; PR00013; FN_Type_II.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 3.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS0231; RICIN_B_LECTIN; 1.
DR Kinase; Receptor.
SQ SEQUENCE 1479 AA; 166654 MW; C7583EA78E2792D1 CRC64;
Query Match 16.0%; Score 176.5; DB 4; Length 1479;
Best Local Similarity 30.4%; Pred. No. 6.7e-08;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;
Oy 5 SGQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRDGGQLVSIKIEKIEFIE 64
Db 385 SWQPF-----QGHYRL-----QAEKRSWQESKACLRGGDLVSIHMALEFITYK 434
Oy 65 NLLPSDGFVIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS---CGSEVCVV 121
Db 435 QEVE---ELWIGL-----NDLKLQMNFEWSGSLVSTHWHPFEPNFRDSDLCVT 483
Oy 122 MYHQSPAGIGGPFYFQNDRCNMKNFICKYDKEKPAVPSRAEG 169
Db 484 IW----GPEG-----RWNDSPCNQSLPSICKAGQLSQGAEEHDHG 520
RESULT 16
Q64449 PRELIMINARY; PRT; 1479 AA.
AC Q64449;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lactin lambda.
GN MRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96355501; PubMed=8702911;
RA Wu K., Yuan J., Lasky L.A.;
RT "Characterization of a novel member of the macrophage mannose receptor
type C lectin family.";
RL J. Biol. Chem. 271:21323-21330(1996).
DR EMBL; U56734; AAC52729.1; -;
DR PUR; T42710; T42710.
DR HSP; P02751; 2FN2.
DR MGD; MGI:107818; MRC2.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006110; P:transport; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR008997; RicinB_Like.
DR InterPro; IPR000772; Ricin_E_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c; 8.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR00013; FN_Type_II.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 3.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS0231; RICIN_B_LECTIN; 1.
DR SEQUENCE 1479 AA; 167112 MW; 62D456E10B9B48C1 CRC64;
Query Match 15.4%; Score 170.5; DB 11; Length 1479;
Best Local Similarity 31.4%; Pred. No. 2.5e-07;
Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;
Oy 5 SGQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRDGGQLVSIKIEKIEFIE 64
Db 384 SWQPF-----QGHYRL-----QAEKRSWQESKACLRGGDLVSIHMALEFITYK 433
Oy 65 NLLPSDGFVIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS---CGSEVCVV 121
Db 434 QEVE---ELWIGL-----NDLKLQMNFEWSGSLVSTHWHPFEPNFRDSDLCVT 482
Oy 122 MYHQSPAGIGGPFYFQNDRCNMKNFICK 154
Db 483 IW----GPEG-----RWNDSPCNQSLPSICK 504
RESULT 17
Q8C4F8 PRELIMINARY; PRT; 217 AA.
AC Q8C4F8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chondroitin sulfate proteoglycan 3 (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 20
Q9XXY3 PRELIMINARY; PRT; 134 AA.
AC Q9XXY3;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Receptor protein-tyrosine kinase (Fragment).
GN HTK28.
OS Hydra magnipapillata (Hydra).
OC Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RX MEDLINE=20209407; PubMed=10744720;
RA Redding J.C., Miller M.A., Steele R.E.;
RT "Sweet Tooth, a Novel Receptor Protein-tyrosine Kinase with C-type
RT Lactin-like Extracellular Domains";
RL J. Biol. Chem. 275:10323-10330(2000).
DR EMBL; AF129528; AAD30040.1; -.
DR HSP; P22897; IEGG.
DR GO; GO:006301; F:kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lactin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Kinase; Tyrosine-protein kinase.
FT NON_TER 1
FT TER 134
SQ SEQUENCE 134 AA; 15701 MW; E7B7211C881009BC CRC64;

Query Match 14.6%; Score 161.5; DB 5; Length 134;
Best Local Similarity 28.8%; Pred. No. 1e-07; Mismatches 23; Indels 25; Gaps 5;
Matches 40; Conservative 23;

Qy 18 CYKVIYFHDTSRLNFEAKACRRDGGQGVLSIESEDEQKLEKFIENLLPSDGFHWGL 77
Db 16 CY--FFQNKTLQAKWRDASLSQALGGHLLSIEDQAEFFLNFLKDSMQQDNYWGL 73
Qy 78 RREKQKNSACQDLYAWTDSISQFRNYYVDEP--CGSEVCVVMYHQPASAGIGGP 135
Db 74 -----NDASNNREFRWSDDIKPQFFNLPKPNDDQEQNCV-----ETNSMG-- 116
Qy 136 YMFQWDDRCNMKNFICK 154
Db 117 -----WNECDATNGFICK 131

RESULT 21
Q8VIF6 PRELIMINARY; PRT; 742 AA.
AC Q8VIF6;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Scavenger receptor with C-type lectin.
GN COLEC12 OR SRCL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21575692; PubMed=11718900;
RA Nakamura K., Funakoshi H., Tokunaga F., Nakamura T.;
RT "Molecular cloning of a mouse scavenger receptor with C-type lectin
RT (SRCU) (1), a novel member of the scavenger receptor family.";
RL Biochim. Biophys. Acta 1522:53-58(2001).

DR EMBL; AB038519; BAB82497.1; -.
DR MGD; MGI:2152907; Colec12.
DR GO; GO:0006955; P:immune response; IDA.
DR GO; GO:0006910; P:phagocytosis, binding; IDA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lactin_C.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Receptor; Lactin.
SQ SEQUENCE 742 AA; 81307 MW; 85A90D3AE881DB6B CRC64;

Query Match 14.4%; Score 159.5; DB 11; Length 742;
Best Local Similarity 33.1%; Pred. No. 1.3e-06; Mismatches 55; Indels 27; Gaps 8;
Matches 49; Conservative 17;

Qy 18 CYKVIYFHDTSRLNFEAKACRRDGGQGVLSIESEDEQKLEKFIENLLPSDGFHWGL 77
Db 618 CY--YF--SLEKEILEDKLFCEKSSHLVFNREEQWIKKH---TVGRESHWIGL 668
Qy 78 RREKQKNSACQDLYAWTDSISQFRNYYVDEP--CGSEVCVVMYHQPASAGIGGP 136
Db 669 TDSEQSE-----WKMLDGSFVYKWKAGQPDNWSG-----HGPEDCA-GLIY 713
Qy 137 MFWNDDRCNMKNFICKYSDKXPVPS 164
Db 714 AGQWDFQCDENNFICE--KEREAVPS 739

RESULT 22
Q8CJ86 PRELIMINARY; PRT; 142 AA.
AC Q8CJ86;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE SIGNR1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Swiss Webster; TISSUE=Skin;
RX MEDLINE=22133304; PubMed=12137941;
RA Parent S.A., Zhang T., Chretien G., Clemen J.A., Figueroa D.J., Ky B.,
RA Blevins R.A., Austin C.P., Rosen H.;
RT "Molecular characterization of the murine SIGNR1 gene encoding a C-
RT type lectin homologous to human DC-SIGN and DC-SIGNR.";
RL Gene 293:33-46(2002).
DR EMBL; AF424802; AAN75597.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lactin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
FT NON_TER 1
FT TER 142
SQ SEQUENCE 142 AA; 16437 MW; 0CB36A383D025EF CRC64;

Query Match 14.3%; Score 158; DB 11; Length 142;
Best Local Similarity 32.4%; Pred. No. 2.4e-07; Mismatches 45; Indels 34; Gaps 9;
Matches 48; Conservative 21;

Qy 23 YEHDTSLNFEAKACRRDGGQGVLSIESEDEQKLEKFIENLLPSDGFHWGLRREE 82
Db 24 YFFSKSOR--NWDNAVTKKVKQLVINSDEEQ----TFLOQTSRAKGTWGLSLDKK 78

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QY 83 KQNSTACODLYAWTGDGI--SQFRN-WYVDEP-SCGSEVCVMYHQPSAPAGIGPYMF 138
Db 79 EAT-----WLWVDGSTLSRFQKYNRGEPNNGEDCVCF-----AGDG----- 118

QY 139 QWDDRCNMKNPFICKYDEKPAVPSRE 166
Db 119 -WNDSKCELKFWICK---KSAATPCTE 141

RESULT 23
Q8BHK7 PRELIMINARY; PRT; 142 AA.
AC Q8BHK7
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SIGNR1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Spleen;
RX MEDLINE=21133304; PubMed=12137941;
RA Parent S.A., Zhang T., Chretien G., Clemas J.A., Figueroa D.J., Ky B.,
RA Blevins R.A., Austin C.P., Rosen H.;
RT "Molecular characterization of the murine SIGNR1 gene encoding a C-
RT type lectin homologous to human DC-SIGN and DC-SIGNR.";
RL Gene 295:33-46(2002).
DR EMBL; AF424800; AAN75595.1; -.
DR EMBL; AF424801; AAN75596.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR Pfam; PF00059; Lectin_C.1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
FT NON_TER
FT 1
SQ SEQUENCE 142 AA; 16471 MW; 0CB36A383D897EF CRC64;

Query Match 14.3%; Score 158; DB 11; Length 142;
Best Local Similarity 32.4%; Pred.No. 2.4e-07;
Matches 48; Conservative 21; Mismatches 45; Indels 34; Gaps 9;

QY 23 YFHTSRLNFEAKACRRDGGQLVSISEDEQKLEKFTENLLPSDGFWIGLRREE 82
Db 24 YFFSKSQ-RNWDVATACKVEKQAQLVIINSDEQ-----TFLOQTSKAKGPTWGLSLDKK 78

QY 83 KQNSTACODLYAWTGDGI--SQFRN-WYVDEP-SCGSEVCVMYHQPSAPAGIGPYMF 138
Db 79 EAT-----WLWVDGSTLSRFQKYNRGEPNNGEDCVCF-----AGDG----- 118

QY 139 QWDDRCNMKNPFICKYDEKPAVPSRE 166
Db 119 -WNDSKCELKFWICK---KSAATPCTE 141

RESULT 24
Q91ZW4 PRELIMINARY; PRT; 295 AA.
AC Q91ZW4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SIGNR1 TM-less isoform.
GN CD209B OR SIGNR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Park C.G., Steinman R.M.;
RT "Alternatively Spliced Forms of Mouse DC-SIGN Homologs.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF374471; AAL27540.1; -.
DR MGD; MGI:1916415; Cd209b.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR Pfam; PF00059; lectin_C.1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 295 AA; 33888 MW; A491F7D3551A91D0 CRC64;

Query Match 14.3%; Score 158; DB 11; Length 295;
Best Local Similarity 32.4%; Pred.No. 5.8e-07;
Matches 48; Conservative 21; Mismatches 45; Indels 34; Gaps 9;

QY 23 YFHTSRLNFEAKACRRDGGQLVSISEDEQKLEKFTENLLPSDGFWIGLRREE 82
Db 177 YFFSKSQ-RNWDVATACKVEKQAQLVIINSDEQ-----TFLOQTSKAKGPTWGLSLDKK 231

QY 83 KQNSTACODLYAWTGDGI--SQFRN-WYVDEP-SCGSEVCVMYHQPSAPAGIGPYMF 138
Db 232 EAT-----WLWVDGSTLSRFQKYNRGEPNNGEDCVCF-----AGDG----- 271

QY 139 QWDDRCNMKNPFICKYDEKPAVPSRE 166
Db 272 -WNDSKCELKFWICK---KSAATPCTE 294

RESULT 25
Q9DBV4 PRELIMINARY; PRT; 311 AA.
AC Q9DBV4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1810030122Rik protein.
GN CD209B OR 1810030122Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21055660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).

```

Search completed: September 9, 2004, 22:56:41
Job time : 72.6769 secs

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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:39:44 ; Search time 85.2999 Seconds
(without alignments)
672.496 Million cell updates/sec

Title: US-087-855-2_COPY_25_227
Perfect score: 1100
Sequence: 1 RLISGVQVCGTQPCYKV.....BEDAKTFKESREALNLAY 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	100.0	374	3 AAY93948	Aay93948 Amino aci
2	1100	100.0	374	4 AAE03651	Aae03651 Human ext
3	1100	100.0	374	5 ABB90203	Abb90203 Human pol
4	1100	100.0	374	5 ABG66680	Abg66680 Human nov
5	1100	100.0	374	6 ADA54522	Ada54522 Human pro
6	1100	100.0	387	4 ARM25796	Arm25796 Human pro
7	1096	99.6	374	6 ADA54574	Ada54574 Human pro
8	1090	99.1	374	3 AAY91490	Aay91490 Human sec
9	1086	98.7	382	2 AAY13367	Aay13367 Amino aci
10	1086	98.7	382	3 ADC78457	Adc78457 Human pro
11	1086	98.7	382	4 AAB80235	Aab80235 Human PRO
12	1086	98.7	382	4 AAU29033	Aau29033 Human PRO
13	1086	98.7	382	6 ABU58409	Abu58409 Human PRO
14	1086	98.7	382	6 ABU71613	Abu71613 Human PRO
15	1086	98.7	382	6 ABUS9757	Abus9757 Novel hum
16	1086	98.7	382	6 ABUS4272	Abus4272 Human sec
17	1086	98.7	382	6 ABR65146	Abr65146 Human sec
18	1086	98.7	382	6 ABR65336	Abr65336 Human sec
19	1086	98.7	382	6 ABU99476	Abu99476 Human PRO
20	1086	98.7	382	6 ABUS92715	Abus92715 Human PRO
21	1086	98.7	382	6 ABUS9836	Abus9836 Novel hum
22	1086	98.7	382	6 ABUS71468	Abus71468 Human PRO
23	1086	98.7	382	6 ABR68085	Abr68085 Human sec
24	1086	98.7	382	6 ABUS9138	Abus9138 Novel hum
25	1086	98.7	382	6 ABUS2569	Abus2569 Human sec

26	1086	98.7	382	6 ABO08646	AbO08646 Human sec
27	1086	98.7	382	6 ABO02698	AbO02698 Human sec
28	1086	98.7	382	6 ABR74852	AbR74852 Human sec
29	1086	98.7	382	6 ABR94614	AbR94614 Human sec
30	1086	98.7	382	6 ABUS5587	AbUS5587 Human PRO
31	1086	98.7	382	6 ABUS98747	AbUS98747 Novel hum
32	1086	98.7	382	6 ABUS97962	AbUS97962 Novel hum
33	1086	98.7	382	6 ABUS1668	AbUS1668 Novel hum
34	1086	98.7	382	6 ABUS71914	AbUS71914 Human sec
35	1086	98.7	382	6 ABUS9361	AbUS9361 Human PRO
36	1086	98.7	382	6 ABUS6202	AbUS6202 Human sec
37	1086	98.7	382	6 ABUS67415	AbUS67415 Human sec
38	1086	98.7	382	6 ABUS0443	AbUS0443 Human PRO
39	1086	98.7	382	6 ABUS01797	AbUS01797 Novel hum
40	1086	98.7	382	6 ABR99361	AbR99361 Human sec
41	1086	98.7	382	6 ABR98751	AbR98751 Human sec
42	1086	98.7	382	6 ABUS16274	AbUS16274 Human sec
43	1086	98.7	382	6 ABR92174	AbR92174 Human sec
44	1086	98.7	382	6 ABUS18815	AbUS18815 Human sec
45	1086	98.7	382	6 ABR78236	AbR78236 Human sec

ALIGNMENTS

RESULT 1
AAY93948
ID AAY93948 standard; protein; 374 AA.
XX AAY93948;
AC AAY93948;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of a lectin ss3939 polypeptide.
XX
KW Human; lectin ss3939; chromosome 11; gene therapy.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..21
FT Domain /note= "signal peptide"
FT Domain 22..227
FT Domain /note= "extracellular coding region"
FT Domain 228..248
FT Domain /note= "predicted transmembrane domain"
FT Domain 249..374
FT Domain /note= "predicted cytoplasmic or intracellular domain"

XX WO2000039296-A1.
XX 06-JUL-2000.
XX
XX 22-DEC-1999; 99NO-US030523.
XX
XX 23-DEC-1998; 98US-0113820P.
XX (IMV) IMMUNEX CORP.
XX Anderson DA;
XX
XX WPI; 2000-452394/39.
XX N-PSDB; AAA57382.
XX
XX ss3939 nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it.
XX
XX Claim 12; Page 8; 73pp; English.
XX
XX The present sequence represents a human lectin ss3939 polypeptide. The polynucleotide sequence is a source of probes, which may be used to identify nucleic acids encoding ss3939 proteins, to identify human chromosome number 11, to map genes on human chromosome number 11, to

CC identify diseases associated with chromosome 11, as single-stranded sense
 CC or antisense oligonucleotides to inhibit expression of polypeptides
 CC encoded by the ss3939 gene, and for gene therapy. The ss3939 polypeptides
 CC may be useful for developing treatments for diseases (none specified)
 CC associated with defective or insufficient amounts of the polypeptides.
 CC The antibodies may be useful for detecting the presence of ss3939
 CC polypeptides
 XX
 SQ Sequence 374 AA;

Query Match 100.0%; Score 1100; DB 3; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103; Indels 0; Gaps 0;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLLSGQVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQGLVSIKLEK 60
 DB 25 RLLSGQVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQGLVSIKLEK 84
 QY 61 FIENLLPSDGFWIGLRREKQNSACQDIYAWTDGSIQFRNYYVDEPSCGSEVCV 120
 DB 85 FIENLLPSDGFWIGLRREKQNSACQDIYAWTDGSIQFRNYYVDEPSCGSEVCV 144
 QY 121 MYHQPAPAGIGGPPYFQWDDRCNKNFNCKYSDKPAVPSREAEGETLTPVLPE 180
 DB 145 MYHQPAPAGIGGPPYFQWDDRCNKNFNCKYSDKPAVPSREAEGETLTPVLPE 204
 QY 181 ETQEDAKKTFKESREAAALNLAY 203
 DB 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 2
 ID AAE03651
 AC AAE03651;
 DT 06-AUG-2001 (first entry)
 DE Human extracellular matrix and cell adhesion molecule-15 (XMAD-15).
 KW Human; extracellular matrix and cell adhesion molecule; XMAD;
 KW gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia;
 KW Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy;
 KW sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
 KW inflammatory disorder; acquired immune deficiency syndrome; AIDS;
 KW Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma;
 KW Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer;
 KW glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis;
 KW osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis;
 KW infection; cell proliferative disorder; actinic keratosis; myeloma;
 KW arteriosclerosis; neutropenic; anticonvulsant; antithyroid; nephrotropic;
 KW neuroprotective; dermatological.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..24 /label= Signal_peptide
 FT Protein 25..374 /note= "Mature human extracellular matrix and cell adhesion molecule (XMAD)"
 FT Domain 46..63 /note= "C-type lectin domain"
 FT Domain 163..176 /note= "C-type lectin domain"
 FT Domain 224..247 /note= "Transmembrane motif"
 FT Domain 328..348 /note= "Transmembrane motif"
 PN WO200142285-A2.

PD 14-JUN-2001.
 XX 05-DEC-2000; 2000WC-US032990.
 PF 10-DEC-1999; 99US-0172852P.
 PR 16-DEC-1999; 99US-0172354P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Yue H, Tang YT, Lal P, Burford N, Azimzai Y, Patterson C;
 PI Baughn MR, Lu DAM, Shah P, Au-Young J;
 XX WPI; 2001-381632/40.
 DR N-PSDB; AAD08039.
 XX New human extracellular matrix and cell adhesion molecules and
 PT polynucleotide sequences encoding them, useful for diagnosis, prevention,
 PT treatment of genetic, autoimmune and cell proliferative disorders.
 XX
 PS Claim 1; Page 108-109; 135pp; English.

CC The present sequence is a human extracellular matrix and cell adhesion
 CC molecule (XMAD). The XMAD is used for screening a compound for
 CC effectiveness as an agonist or antagonist of XMAD. The identified agonist
 CC or antagonist are used for treating a disease or condition associated
 CC with decreased or increased expression of functional XMAD. The
 CC polynucleotides encoding XMAD are useful in somatic or germline gene
 CC therapy to correct a genetic deficiency, to express a conditionally
 CC lethal gene product and to express a protein which affords protection
 CC against intracellular parasites and also for diagnosis of disorders
 CC associated with expression of XMAD. They are also used for generating
 CC hybridisation probes useful in mapping the naturally occurring genomic
 CC sequences and to create knock in humanised animals (pigs) or transgenic
 CC animals (mice or rats) to model human diseases. Oligonucleotide or longer
 CC fragments derived from the polynucleotide sequences may be used as
 CC elements on a microarray. Antibodies which specifically bind XMAD may be
 CC used for the diagnosis of disorders associated with the expression of
 CC XMAD, or in assays to monitor patients being treated with XMAD. Diseases
 CC diagnosed, prevented or treated include genetic disorders such as
 CC adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's
 CC disease, myotonic dystrophy, sickle cell anaemia, thalassaemia,
 CC autoimmune/inflammatory disorders such as acquired immune deficiency
 CC syndrome (AIDS), Addison's disease, allergies, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, diabetes mellitus, atopic dermatitis,
 CC glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthritis,
 CC osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis,
 CC bacterial, fungal, parasitic, protozoal and helminthic infections and
 CC cell proliferative disorders such as actinic keratosis, arteriosclerosis
 CC and cancer including breast, bladder, bone marrow, brain and uterus
 CC cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma
 XX
 SQ Sequence 374 AA;

Query Match 100.0%; Score 1100; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103; Indels 0; Gaps 0;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLLSGQVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQGLVSIKLEK 60
 DB 25 RLLSGQVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQGLVSIKLEK 84
 QY 61 FIENLLPSDGFWIGLRREKQNSACQDIYAWTDGSIQFRNYYVDEPSCGSEVCV 120
 DB 85 FIENLLPSDGFWIGLRREKQNSACQDIYAWTDGSIQFRNYYVDEPSCGSEVCV 144
 QY 121 MYHQPAPAGIGGPPYFQWDDRCNKNFNCKYSDKPAVPSREAEGETLTPVLPE 180
 DB 145 MYHQPAPAGIGGPPYFQWDDRCNKNFNCKYSDKPAVPSREAEGETLTPVLPE 204
 QY 181 ETQEDAKKTFKESREAAALNLAY 203
 DB 205 ETQEDAKKTFKESREAAALNLAY 227

QY 121 MYHQSAPAGIGGYPYFQWDDRCNNKNFNICKYSDKPAVPSREAGEETELTTTPVLPE 180
DB 145 MYHQSAPAGIGGYPYFQWDDRCNNKNFNICKYSDKPAVPSREAGEETELTTTPVLPE 204
QY 181 ETQEDAKKTFKESREAAALNLAY 203
DB 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 4
ABG66680
ID ABG66680 standard; protein; 374 AA.
XX
AC ABG66680;
DT 30-AUG-2002 (first entry)
XX
DE Human novel polypeptide #15.
XX
KW Human; inflammatory condition; shock; sepsis; immune response; cancer;
KW wound healing; central nervous system disease; haematopoiesis;
KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
KW bone degenerative disorder; periodontal disease; reperfusion injury;
KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
KW allergic condition; thrombolysis; thrombosis; coagulation disorder;
KW fungal infection.
XX
OS Homo sapiens.
XX
PN WO200244340-A2.
XX
PD 06-JUN-2002.
XX
XX 30-NOV-2001; 2001WO-US047004.
XX
XX 30-NOV-2000; 2000US-00728952.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
XX Yamazaki V, Ujwal ML, Drmanac RT;
PI
XX WPI; 2002-508509/54.
XX N-PSDB; ABK94904.
XX
XX Novel nucleic acids and polypeptides for diagnosis, treatment of
XX inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
XX disorders, cancer and promoting wound healing.
XX
XX Claim 10; Page 579-580; 672pp; English.
XX
XX The invention relates to human novel polynucleotides and associated
XX polypeptides. The polynucleotides and polypeptides are useful for
XX treating inflammatory conditions such as arthritis, nephritis, Crohn's
XX disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
XX and cancer and for promoting wound healing. The sequences are used to
XX induce the proliferation of neural cells and regeneration of nerve and
XX brain tissue, and are useful for the treatment of central and peripheral
XX nervous system diseases and neuropathies, such as Alzheimer's disease,
XX Parkinson's disease, Huntington's disease and amyotrophic lateral
XX sclerosis. The sequences are involved in chemotactic or chemokinetic
XX activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
XX cell disorders and platelet disorders such as thrombocytopenia,
XX regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
XX growth, tissue repair, healing of burns, incisions, ulcers, treatment of
XX osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
XX disease. The sequences of the invention are also useful for gut
XX protection or regeneration and treatment of lung or liver fibrosis,
XX reperfusion injury in various tissues, immune deficiencies and disorders
XX including severe combined immunodeficiency (SCID), bacterial or fungal
XX infections, autoimmune disorders e.g. multiple sclerosis and myasthenia

QY 121 MYHQSAPAGIGGYPYFQWDDRCNNKNFNICKYSDKPAVPSREAGEETELTTTPVLPE 180
DB 145 MYHQSAPAGIGGYPYFQWDDRCNNKNFNICKYSDKPAVPSREAGEETELTTTPVLPE 204
QY 181 ETQEDAKKTFKESREAAALNLAY 203
DB 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 3
ABB90203
ID ABB90203 standard; protein; 374 AA.
XX
AC ABB90203;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2579.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-US016450.
XX
XX 19-MAY-2000; 2000US-0205515P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-122018/16.
XX N-PSDB; ABL90612.
XX
XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
XX prevention of neural, immune system, muscular, reproductive,
XX gastrointestinal, pulmonary, cardiovascular, renal and proliferative
XX disorders.
XX
XX Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABL90449-ABL90853) and proteins
XX (ABB90440-ABB90444) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
XX breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX cardiovascular disorders such as myocardial ischaemia; and (f)
XX ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX infectious diseases such as viral, bacterial, fungal and parasitic
XX infections. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 374 AA;
XX
XX Query Match 100.0%; Score 1100; DB 5; Length 374;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-103;
XX Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 RLLSQPVCGTQPCVKYVYFHTTSRLNFEFAKEACRRDGGQLVISEDQKLEK 60
DB 25 RLLSQPVCGTQPCVKYVYFHTTSRLNFEFAKEACRRDGGQLVISEDQKLEK 84
QY 61 FIENLLPSDGFWIGLRREKQSNSTACODLIYAMTDGSIQFRNWWYDEPSCSEVCV 120
DB 85 FIENLLPSDGFWIGLRREKQSNSTACODLIYAMTDGSIQFRNWWYDEPSCSEVCV 144

CC gravis, allergic conditions such as asthma, thrombolysis or thrombosis
 CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human
 CC novel polypeptides of the invention
 XX
 SQ Sequence 374 AA;

Query Match 100.0%; Score 1100; DB 5; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGPVCRCGTQPCYKVIYFHDTSRLNFEAEACRRDGGQLVSI ESEDEQKLIK 60
 DB 25 RLLSGPVCRCGTQPCYKVIYFHDTSRLNFEAEACRRDGGQLVSI ESEDEQKLIK 84
 QY 61 FIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPSCGSEVCV 120
 DB 85 FIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPSCGSEVCV 144
 QY 121 MYHQPAPAGIGGPFYFQWDDRCNKNFNICKYSDKPAVPSREAGEETELTPVLPE 180
 DB 145 MYHQPAPAGIGGPFYFQWDDRCNKNFNICKYSDKPAVPSREAGEETELTPVLPE 204
 QY 181 ETQEDAKTKFKESREAAALNLAY 203
 DB 205 ETQEDAKTKFKESREAAALNLAY 227

RESULT 5
 ADA54522
 ID ADA54522 standard; protein; 374 AA.
 XX
 AC ADA54522;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human protein, SEQ ID 2090.
 XX
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX
 OS Homo sapiens.
 XX
 EN EP1293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 XX (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX

XX Isoqai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA52883.
 XX
 XX New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 14; SEQ ID NO 2090; 205pp; English.

XX The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins and/or cancer.

XX
 SQ Sequence 374 AA;
 Query Match 100.0%; Score 1100; DB 6; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGPVCRCGTQPCYKVIYFHDTSRLNFEAEACRRDGGQLVSI ESEDEQKLIK 60
 DB 25 RLLSGPVCRCGTQPCYKVIYFHDTSRLNFEAEACRRDGGQLVSI ESEDEQKLIK 84
 QY 61 FIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPSCGSEVCV 120
 DB 85 FIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPSCGSEVCV 144
 QY 121 MYHQPAPAGIGGPFYFQWDDRCNKNFNICKYSDKPAVPSREAGEETELTPVLPE 180
 DB 145 MYHQPAPAGIGGPFYFQWDDRCNKNFNICKYSDKPAVPSREAGEETELTPVLPE 204
 QY 181 ETQEDAKTKFKESREAAALNLAY 203
 DB 205 ETQEDAKTKFKESREAAALNLAY 227

RESULT 6
 AAM25796
 ID AAM25796 standard; protein; 387 AA.
 XX
 AC AAM25796;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:1311.
 XX
 KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; viricide;
 KW anti-HIV; fungicide; antitumor; cardiovascular; antianemic; anaemia;
 KW antitumor; haemostatic; vulnery; antidiabetic; osteopathic; eczema;
 KW dermatological; antiallergic; antisthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder.

XX Homo sapiens.
 OS
 XX WO200153455-A2.
 EN
 XX 26-JUL-2001.
 PD
 XX 22-DEC-2000; 2000WO-US035017.
 PF
 XX 23-DEC-1999; 99US-00471275.
 PR
 XX 21-JAN-2000; 2000US-00488725.
 PR
 XX 25-APR-2000; 2000US-00552317.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-457603/49.
 DR
 XX N-PSDB; AAH59737.

XX Isolated human polynucleotides encoding polypeptides, useful for the
 CC treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
 CC

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 CC AAM25963. The proteins can have activities based on the tissues and cells
 CC they are expressed in, such as: anti-inflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; anaemic; antaggregant; haemostatic; vulnerary;
 CC antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmune, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders
 XX SQ Sequence 387 AA;

Query Match 100.0%; Score 1100; DB 4; Length 387;
 Best Local Similarity 100.0%; Pred. No. 1.4e-103; Indels 0; Gaps 0;
 Matches 203; Conservative 0; Mismatches 0;
 Qy 1 RLLSGQPCVCGTQPCYKVIYFHDTSRLNFEAKACRRDGGQVLSIESDEQKLIK 60
 Db 38 RLLSGQPCVCGTQPCYKVIYFHDTSRLNFEAKACRRDGGQVLSIESDEQKLIK 97
 Qy 61 FIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 120
 Db 98 FIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 157
 Qy 121 MYHQPAPAGIGGPFYFQWDDRCNMKNFICKYSDKPAVPSRAEGEETELTPVLPE 180
 Db 158 MYHQPAPAGIGGPFYFQWDDRCNMKNFICKYSDKPAVPSRAEGEETELTPVLPE 217
 Qy 181 ETQEDAKTKFKESREAAALNLAY 203
 Db 218 ETQEDAKTKFKESREAAALNLAY 240

RESULT 7
 ADA54574
 ID ADA54574 standard; protein; 374 AA.
 AC ADA54574;
 DT 20-NOV-2003 (first entry)
 DE Human protein, SEQ ID 2142.
 XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX Homo sapiens.
 OS Homo sapiens.
 PN EP1293569-A2.
 XX 19-MAR-2003.
 PD 21-MAR-2002; 2002EP-00006586.
 XX 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-395539/38.
 DR N-PSDB; ADA52935.
 XX New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX Claim 14; SEQ ID NO 2142; 205pp; English.
 PS The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 XX SQ Sequence 374 AA;

Query Match 99.8%; Score 1096; DB 6; Length 374;
 Best Local Similarity 99.5%; Pred. No. 3.4e-103;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RLLSGQPCVCGTQPCYKVIYFHDTSRLNFEAKACRRDGGQVLSIESDEQKLIK 60
 Db 25 RLLSGQPCVCGTQPCYKVIYFHDTSRLNFEAKACRRDGGQVLSIESDEQKLIK 84
 Qy 61 FIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 120
 Db 85 FIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 144
 Qy 121 MYHQPAPAGIGGPFYFQWDDRCNMKNFICKYSDKPAVPSRAEGEETELTPVLPE 180
 Db 145 MYHQPAPAGIGGPFYFQWDDRCNMKNFICKYSDKPAVPSRAEGEETELTPVLPE 204
 Qy 181 ETQEDAKTKFKESREAAALNLAY 203
 Db 205 ETQEDAKTKFKESREAAALNLAY 227

RESULT 8
 AAY91490
 ID AAY91490 standard; protein; 374 AA.
 AC AAY91490;
 DT 29-JUN-2000 (first entry)
 DE Human secreted protein sequence encoded by gene 40 SEQ ID NO:163.
 XX Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
 KW antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
 KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
 KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
 KW immune disease; inflammation; blood disorder; tumour.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200006698-A1.
 XX 10-FEB-2000.
 PD 29-JUL-1999; 99WO-US017130.
 XX 30-JUL-1998; 98US-0094657P.
 PR 05-AUG-1998; 98US-0095486P.
 PR 06-AUG-1998; 98US-0095454P.
 PR 06-AUG-1998; 98US-0095455P.
 PR 12-AUG-1998; 98US-0096319P.

PA (HUMA-) HUMAN GENOME SCI INC.
XX Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX WPI: 2000-195282/17.
DR N-PSDB; AA26385.
XX New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX Claim 11; Page 483-484; 634pp; English.
XX The polynucleotide sequences given in AAA26346 to AAA26458 encode the
CC human secreted proteins given in AA91451 to AA91691. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic;
CC immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;
CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
CC asthma; antiparasitic; and cardiant. The polynucleotides and their
CC corresponding secreted proteins are useful for preventing, treating or
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
CC pathological conditions can be diagnosed by determining the amount of the
CC proteins in a sample or by determining the presence of mutations in the
CC polynucleotides. Specific uses are described for each of the
CC polynucleotides, based on which tissues they are most highly expressed
CC in, and include developing products for the diagnosis or treatment of
CC cancer, tumors, neurodegenerative disorders, developmental abnormalities
CC and foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,
CC Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
CC reproductive disorders, gastrointestinal disorders, respiratory disorders
CC and metabolic disorders. The proteins or polynucleotides can also be used
CC as food additives or preservatives. The proteins are also useful for
CC identifying their binding partners. AAA26337 to AAA26345 and AA91450 are
CC sequences used in the exemplification of the present invention
XX Sequence 374 AA;
XX
XX Query Match 99.1%; Score 1090; DB 3; Length 374;
XX Best Local Similarity 99.0%; Pred. No. 1.4e-102;
XX Matches 201; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 RLSSQPCVCRGTQPCVKVIYFHTSRLNFEAKEACRRDGGQVLSIEDEKQLEK 60
XX 25 RLSSQPCVCRGTQPCVKVIYFHTSRLNFEAKEACRRDGGQVLSIEDEKQLEK 84
XX 61 FIENLLPSDGDGFWIGLRREERKQSNSTACQDLYAWTDGSIQCFRNWYVDEPSCGSEVCV 120
XX 85 FIENLLPSDGDGFWIGLRREERKQSNSTACQDLYAWTDGSIQCFRNWYVDEPSCGSEVCV 144
XX 121 MYHQSAPAGICGGPYNFWNDRCNKNKFNICKYSDEKPAVPSREAGEETELTTPVLPE 180
XX 145 MYHQSAPAGICGGPYNFWNDRCNKNKFNICKYSDEKPAVPSREAGEETELTTPVLPE 204
XX 181 ETQEDAKKTFKESREAAINLAY 203
XX 205 ETQEDAKKTFKESREAAINLAY 227
XX
XX RESULT 9
XX ID AA913367
XX AC AA913367;
XX DT 25-JUN-1999 (first entry)
XX

XX Secreted protein; transmembrane protein; human; enterocolitis;
XX Zollinger-Ellison syndrome; gastrointestinal ulceration;
XX congenital microvillus atrophy; skin disease; cell growth;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
XX dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
XX wound healing; tissue repair.
XX Homo sapiens.
XX WO9914328-A2.
XX 25-MAR-1999.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059117P.
XX 17-SEP-1997; 97US-0059119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 17-OCT-1997; 97US-0062287P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063045P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
XX 27-OCT-1997; 97US-0063327P.
XX 27-OCT-1997; 97US-0063329P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
XX 28-OCT-1997; 97US-0063550P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063732P.
XX 29-OCT-1997; 97US-0063734P.
XX 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
XX 31-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
XX 03-NOV-1997; 97US-0064248P.
XX 07-NOV-1997; 97US-0064809P.
XX 12-NOV-1997; 97US-0065186P.
XX 17-NOV-1997; 97US-0065846P.
XX 18-NOV-1997; 97US-0065693P.
XX 21-NOV-1997; 97US-0066120P.
XX 21-NOV-1997; 97US-0066364P.
XX 24-NOV-1997; 97US-0066453P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066511P.
XX 24-NOV-1997; 97US-0066770P.
XX 24-NOV-1997; 97US-0066772P.
XX 25-NOV-1997; 97US-0066840P.
XX (GETH) GENENTECH INC.
XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
XX

DR N-PSDB; AAX52238.

XX New isolated human genes and polypeptides used in, e.g. treatment of

PT gastrointestinal ulceration.

XX

PS Claim 12; Fig 50; 320pp; English.

XX

AAV1344-403 represent secreted and transmembrane human proteins. The

CC cDNA sequences are obtained from cDNA libraries, prepared from fetal

CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The

CC encoded polypeptides have specific uses based on their homology to known

CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated

CC with the preservation and maintenance of gastrointestinal mucosa and the

CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,

CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital

CC microvillus atrophy), skin diseases associated with abnormal keratinocyte

CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous

CC cell carcinoma of the vulva and gliomas), potent effects on cell growth

CC and development, diseases related to growth or survival of nerve cells

CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or

CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal

CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may

CC be used in the treatment of Usher Syndrome or Atrophia areata. PRO269 can

CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may

CC have therapeutic applications in wound healing and tissue repair; PRO317

CC can be used for treating problems of the kidney, uterus, endometrium,

CC blood vessels, or related tissue, e.g. in the heart of genital tract

XX

SQ Sequence 382 AA;

Query Match 98.7%; Score 1086; DB 2; Length 382;

Best Local Similarity 96.2%; Pred. No. 3.7e-102;

Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQPCVCGGTQPCYKVIYFHDTSRLNFEFAKEACRRDGGQLVSIIESE 52

DB 25 RLLSASDLDRGGQPCVCGGTQPCYKVIYFHDTSRLNFEFAKEACRRDGGQLVSIIESE 84

QY 53 DEQKLIETFIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 112

DB 85 DEQKLIETFIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 144

QY 113 CGSEVCVMVHQPAPAGIGGYPWFQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 172

DB 145 CGSEVCVMVHQPAPAGIGGYPWFQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 204

QY 173 LTTPLPEETQEDAKKTFKESREAAALNLAY 203

DB 205 LTTPLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 10

ID ADC78457

XX ADC78457 standard; protein; 382 AA.

XX

AC ADC78457;

XX

DT 01-JAN-2004 (first entry)

XX

DE Human PRO234 protein.

XX

antifungal; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;

KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;

KW neurotrophic; osteopathic; antiaesthetic; antiarthritic; antirheumatic;

KW antiatherosclerotic; cardiac; antidiabetic; cerebroprotective; syndrome;

KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;

KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;

KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;

KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;

KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;

KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;

KW diabetes; stroke; gene therapy; transgenic; PRO; human.

OS Homo sapiens.

XX

PN WO200015796-A2.

XX

PD 23-MAR-2000.

XX

PF 15-SEP-1999; 99WO-US021090.

XX

PR 16-SEP-1998; 98WO-US019330.

XX

PA (GETH) GENENTECH INC.

XX

PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;

PI Yuan J;

XX

DR WPI: 2000-271434/23.

DR N-PSDB; ADC78456.

XX

PT Novel nucleic acids encoding secreted and transmembrane polypeptides with

PT homology, e.g. to growth and cancer-associated antigens.

XX

PS Claim 12; SEQ ID NO 137; 355pp; English.

XX

CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.

CC The polypeptides and polynucleotides of the invention may be useful as

CC research tools and as therapeutics for treating enterocolitis, Zollinger-

CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,

CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal

CC scarring and wound healing, nerve repair, thrombosis, bone and/or

CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple

CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,

CC infertility, premature aging, AIDS, diabetes complications and stroke.

CC The molecules may also be utilised during gene therapy procedures and

CC transgenic animal production. The current sequence is that of the human

CC PRO protein of the invention.

XX

SQ Sequence 382 AA;

Query Match 98.7%; Score 1086; DB 3; Length 382;

Best Local Similarity 96.2%; Pred. No. 3.7e-102;

Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQPCVCGGTQPCYKVIYFHDTSRLNFEFAKEACRRDGGQLVSIIESE 52

DB 25 RLLSASDLDRGGQPCVCGGTQPCYKVIYFHDTSRLNFEFAKEACRRDGGQLVSIIESE 84

QY 53 DEQKLIETFIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 112

DB 85 DEQKLIETFIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 144

QY 113 CGSEVCVMVHQPAPAGIGGYPWFQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 172

DB 145 CGSEVCVMVHQPAPAGIGGYPWFQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 204

QY 173 LTTPLPEETQEDAKKTFKESREAAALNLAY 203

DB 205 LTTPLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 11

AAAB80235

ID AAAB80235 standard; protein; 382 AA.

XX

AC AAAB80235;

XX

DT 24-APR-2001 (first entry)

XX

DE Human PRO234 protein.

XX

Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;

KW antiparkinsonian neurotropic; neuroprotective; vulnery; cardiant;

KW angiogenic; vasotropic; antiaesthetic; antirheumatic; cancer;

KW antiarthritic; antiinfectivity; antidiabetic; antiviral; diabetes;

ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
ischaemia; inflammation.

Homo sapiens.
WO200104311-A1.
18-JAN-2001.

22-FEB-2000; 2000WO-US004414.

07-JUL-1999; 99US-0143048P.
26-JUL-1999; 99US-0145698P.
28-JUL-1999; 99US-0146222P.
08-SEP-1999; 99WO-US020524.
13-SEP-1999; 99WO-US020944.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
05-OCT-1999; 99WO-US023089.
29-NOV-1999; 99WO-US028214.
30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028524.
02-DEC-1999; 99WO-US028585.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.

(GETH) GENENTECH INC.

Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Williams PM, Wood WI;

WPI: 2001-081051/09.
N-PSDB; AAF72396.

Sixty one nucleic acids encoding PRO polypeptides which are useful in the
treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
disease).

Claim 1; Fig 50; 393pp; English.

The present sequence is one of sixty one novel secreted and transmembrane
PRO polypeptides. The PRO polypeptides are useful for treating skin
diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
infertility, AIDS and diabetes and retinal disorders such as retinitis
pigmentosa. The PRO nucleic acids have applications in molecular
biology, including use as hybridization probes, and in chromosome and
gene mapping

Sequence 382 AA;

Query Match 98.7%; Score 1086; DB 4; Length 382;
Best Local Similarity 96.2%; Pred No. 3.7e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

1 RLLS-----GQVRCGGTQPCYKVIYFHTSRLNFEAKACRRDGGQLVSIIE 52
25 RLLSASDLRLGGQVRCGGTQPCYKVIYFHTSRLNFEAKACRRDGGQLVSIIE 84
53 DEQKLEFIENLLPSDGFMTGLRRREKOSNSTACQDLYATDGSISQFRNMYVDEPS 112
85 DEQKLEFIENLLPSDGFMTGLRRREKOSNSTACQDLYATDGSISQFRNMYVDEPS 144

QY 113 CGSEVCVMYHOPSPAGIGGPFYQWDDRCNMKNFKYSDKPAVPSREASGEETE 172
Db |||||
QY 145 CGSEVCVMYHOPSPAGIGGPFYQWDDRCNMKNFKYSDKPAVPSREASGEETE 204
Db |||||
QY 173 LTPVLPETQBEDAKKTFKESREAAALNAY 203
Db |||||
QY 205 LTPVLPETQBEDAKKTFKESREAAALNAY 235
Db |||||

RESULT 12

AAU29033

ID AAU29033 standard; protein; 382 AA.

AC AAU29033;

DT 18-DEC-2001 (first entry)

DE Human PRO polypeptide sequence #10.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

OS Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 06-MAR-2000; 2000US-0186968P.

XX 14-MAR-2000; 2000US-0189320P.

XX 14-MAR-2000; 2000US-0189328P.

XX 15-MAR-2000; 2000WO-US006884.

XX 21-MAR-2000; 2000US-0190828P.

XX 21-MAR-2000; 2000US-0191007P.

XX 21-MAR-2000; 2000US-0191048P.

XX 21-MAR-2000; 2000US-0191314P.

XX 28-MAR-2000; 2000US-0192655P.

XX 29-MAR-2000; 2000US-0193032P.

XX 29-MAR-2000; 2000US-0193053P.

XX 30-MAR-2000; 2000WO-US008439.

XX 04-APR-2000; 2000US-0194449P.

XX 04-APR-2000; 2000US-0194647P.

XX 11-APR-2000; 2000US-0195975P.

XX 11-APR-2000; 2000US-0196003P.

XX 11-APR-2000; 2000US-0196187P.

XX 11-APR-2000; 2000US-0196909P.

XX 11-APR-2000; 2000US-0196820P.

XX 18-APR-2000; 2000US-0198121P.

XX 18-APR-2000; 2000US-0198585P.

XX 25-APR-2000; 2000US-0199397P.

XX 25-APR-2000; 2000US-0199550P.

XX 25-APR-2000; 2000US-0199654P.

XX 03-MAY-2000; 2000US-0201516P.

XX 17-MAY-2000; 2000WO-US013705.

XX 22-MAY-2000; 2000WO-US014042.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-2000; 2000WO-US015264.

XX 05-JUN-2000; 2000US-0209832P.

XX 28-JUL-2000; 2000WO-US020710.

XX 28-AUG-2000; 2000US-00644848.

XX 24-AUG-2000; 2000WO-US023328.

XX 08-NOV-2000; 2000WO-US030952.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000WO-US034956.

(GETH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-602746/68.
DR N-ESDB; AAS45934.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX Claim 11; Fig 20; 774pp; English.
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
XX Sequence 382 AA;
Query Match 98.7%; Score 1086; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.7e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
Qy 1 RLIS-----GQVCRGGTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSTSE 52
Db 25 RLLSASDLRLKGGQPCVCKGQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSTSE 84
Qy 53 DEQKLEKFIENLLPDSGDFWIGLRRREEKQNSTACQDLYAWTDGSIQFRNMYVDEPS 112
Db 85 DEQKLEKFIENLLPDSGDFWIGLRRREEKQNSTACQDLYAWTDGSIQFRNMYVDEPS 144
Qy 113 CGSEVCVVMYHQPAPAGIGGPFYFQWDDRCNNKNNFIKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCVVMYHQPAPAGIGGPFYFQWDDRCNNKNNFIKYSDEKPAVPSREAEGETE 204
Qy 173 LTTVPVPEETQEDAKTFKESREAAALNAY 203
Db 205 LTTVPVPEETQEDAKTFKESREAAALNAY 235
RESULT 13
ABU58409
ID ABU58409 standard; protein; 382 AA.
XX AC ABU58409;
XX DT 15-APR-2003 (first entry)
XX DE Human PRO polypeptide #10.
XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX

21-JUN-2002; 2002US-00176492.
18-SEP-1997; 97US-0059263P.
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QY 173 LTPVLPETQEDAKTFKESREALNLAY 203
Db 205 LTPVLPETQEDAKTFKESREALNLAY 235
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AC ABU71613;
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DT 16-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #24.
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KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW pathological disorder; cardiac insufficiency disorder; protein secretion;
KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;

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KW cytotstatic; cardiant; endocrine; antidiabetic; gastrointestinal; antiulcer; dermatological; vulnerary.

XX Homo sapiens.

PN US2002146709-A1.

PD 10-OCT-2002.

PF 18-JUL-2001; 2001US-00909088.

XX 17-SEP-1997; 97US-0059113P.
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PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Flvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-328338/31.
DR N-PSDB; ACA59008.

Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.

Claim 12; Fig 50; 473pp; English.

The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polynucleotides encoding them. The PRO polypeptides and polynucleotides can be used in treating pathological disorders and tumors, in therapeutic treatment of cardiac insufficiency disorders and in therapeutic treatment of disorders involving protein secretion by the pancreas, including diabetes. They can also be used in treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, and skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriasis, epithelial cancers such as lung squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas). The sequences can be used as molecular markers for protein electrophoresis purposes and can be utilised in protein-protein binding assays, biochemical screening assays, immunoassays and cell-based assays. This sequence represents a human PRO polypeptide of the invention

Sequence 382 AA;

Query Match 98.7%; Score 1086; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.7e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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Qy 173 LTTVLPEETQEDAKKTFKESREALNLAY 203
Db 205 LTTVLPEETQEDAKKTFKESREALNLAY 235

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ID ABU87957 standard; protein; 382 AA.
XX AC ABU87957;
XX DT 07-JUL-2003 (first entry)
XX DE
XX DE Novel human secreted and transmembrane protein PRO234.
XX Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
XX PN
XX PN US2003032127-A1.
XX PD
XX PD 13-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183012.
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PR 26-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091353P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
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PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0095012P.

PR 17-AUG-1998; 98US-0096757P.
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 PR 18-AUG-1998; 98US-0096959P.
 PR 18-AUG-1998; 98US-0097022P.
 PR 26-AUG-1998; 98US-0097952P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097955P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097974P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 02-SEP-1998; 98US-0098803P.
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 PR 09-SEP-1998; 98US-0099602P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 15-SEP-1998; 98US-0099812P.
 PR 16-SEP-1998; 98US-0100388P.
 PR 16-SEP-1998; 98US-0100682P.
 PR 16-SEP-1998; 98US-0100684P.
 PR 16-SEP-1998; 98US-0101751P.
 PR 16-SEP-1998; 98US-0101751P.
 PR 17-SEP-1998; 98US-01019330.
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 PR 24-SEP-1998; 98US-0101922P.
 PR 25-SEP-1998; 98US-0101786P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
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 PR 30-SEP-1998; 98US-0102487P.
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 PR 30-SEP-1998; 98US-0102571P.
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 PR 06-OCT-1998; 98US-0103258P.

Query Match 98.7%; Score 1086; DB 6; Length 382;

Best Local Similarity 96.2%; Pred No. 3.7e-102;

Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYPHDTSRRNFEEAKACRRDGGQLVSIIESE 52
 DB 25 RLLSASDLRLGCGQVCRGGTQPCYKVIYPHDTSRRNFEEAKACRRDGGQLVSIIESE 84
 QY 53 DEOKLIEFIENLLSDGDFWIGLRRREKQSNSTACODLYAWTDGSIQFRNMYVDEPS 112
 DB 85 DEOKLIEFIENLLSDGDFWIGLRRREKQSNSTACODLYAWTDGSIQFRNMYVDEPS 144
 QY 113 CGSEVCVMYHQPAPAGITGGPFYMFQWDDRCNMKNFICKYSDKPAVPREAGEETE 172
 DB 145 CGSEVCVMYHQPAPAGITGGPFYMFQWDDRCNMKNFICKYSDKPAVPREAGEETE 204

QY 173 LTTPVLPESTQBEDAKTKFKESREALNLAY 203
 DB 205 LTTPVLPESTQBEDAKTKFKESREALNLAY 235
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 ID AB084272 standard; protein; 382 AA.
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 AC AB084272;
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 DT 02-AUG-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein (PRO) #10.
 XX
 KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing.
 XX
 OS Homo sapiens.
 XX
 PN US2003032112-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 21-JUN-2002; 2002US-00176756.
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 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080194P.
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 PR 22-APR-1998; 98US-0082797P.
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 PR 29-APR-1998; 98US-0083559P.
 PR 05-MAY-1998; 98US-0084366P.

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PR	02-JUN-1998;	98US-0087753P.	PR	26-AUG-1998;	98US-0097971P.
PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097974P.
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PR	04-JUN-1998;	98US-0088028P.	PR	01-SEP-1998;	98US-0098716P.
PR	04-JUN-1998;	98US-0088029P.	PR	01-SEP-1998;	98US-0098723P.
PR	04-JUN-1998;	98US-0088033P.	PR	02-SEP-1998;	98US-0098803P.
PR	04-JUN-1998;	98US-0088326P.	PR	02-SEP-1998;	98US-0098821P.
PR	05-JUN-1998;	98US-0088167P.	PR	02-SEP-1998;	98US-0098843P.
PR	05-JUN-1998;	98US-0088202P.	PR	03-SEP-1998;	98US-0099602P.
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PR	05-JUN-1998;	98US-0088217P.	PR	10-SEP-1998;	98US-0099754P.
PR	09-JUN-1998;	98US-0088655P.	PR	10-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-0088722P.	PR	10-SEP-1998;	98US-0099812P.
PR	10-JUN-1998;	98US-0088738P.	PR	12-SEP-1998;	98US-0100388P.
PR	10-JUN-1998;	98US-0088740P.	PR	16-SEP-1998;	98US-0100662P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100664P.
PR	10-JUN-1998;	98US-0088824P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088825P.	PR	16-SEP-1998;	98US-0101933Q.
PR	10-JUN-1998;	98US-0088826P.	PR	17-SEP-1998;	98US-0100683P.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100684P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100919P.
PR	11-JUN-1998;	98US-0088867P.	PR	17-SEP-1998;	98US-0100930P.
PR	12-JUN-1998;	98US-0089090P.	PR	18-SEP-1998;	98US-0100849P.
PR	12-JUN-1998;	98US-0089105P.	PR	18-SEP-1998;	98US-0101014P.
PR	16-JUN-1998;	98US-0089512P.	PR	18-SEP-1998;	98US-0101068P.
PR	16-JUN-1998;	98US-0089514P.	PR	23-SEP-1998;	98US-0101471P.
PR	17-JUN-1998;	98US-0089538P.	PR	23-SEP-1998;	98US-0101472P.
PR	17-JUN-1998;	98US-0089598P.	PR	23-SEP-1998;	98US-0101475P.
PR	17-JUN-1998;	98US-0089653P.	PR	23-SEP-1998;	98US-0101477P.
PR	18-JUN-1998;	98US-0089908P.	PR	24-SEP-1998;	98US-0101738P.
PR	19-JUN-1998;	98US-0089952P.	PR	24-SEP-1998;	98US-0101739P.
PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101743P.
PR	22-JUN-1998;	98US-0090252P.	PR	24-SEP-1998;	98US-0101922P.
PR	22-JUN-1998;	98US-0090254P.	PR	25-SEP-1998;	98US-0101786P.
PR	24-JUN-1998;	98US-0090428P.	PR	29-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090435P.	PR	29-SEP-1998;	98US-0102240P.
PR	24-JUN-1998;	98US-0090444P.	PR	29-SEP-1998;	98US-0102330P.
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PR	24-JUN-1998;	98US-0090533P.	PR	30-SEP-1998;	98US-0102487P.
PR	25-JUN-1998;	98US-0090540P.	PR	30-SEP-1998;	98US-0102570P.
PR	25-JUN-1998;	98US-0090676P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090678P.	PR	01-OCT-1998;	98US-0102684P.
PR	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102687P.
PR	25-JUN-1998;	98US-0090690P.	PR	02-OCT-1998;	98US-0102965P.
PR	25-JUN-1998;	98US-0090694P.	PR	06-OCT-1998;	98US-0103258P.
PR	25-JUN-1998;	98US-0090695P.	PR	06-OCT-1998;	98US-0103449P.
PR	26-JUN-1998;	98US-0090696P.	PR	07-OCT-1998;	98US-00168978.
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PR	26-JUN-1998;	98US-0090862P.			
PR	26-JUN-1998;	98US-0090863P.			
PR	26-JUN-1998;	98US-0091010P.			
PR	01-JUL-1998;	98US-0091359P.			
PR	01-JUL-1998;	98US-0091544P.			
PR	02-JUL-1998;	98US-0091478P.			
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PR	24-JUL-1998;	98US-0094006P.			

Query Match 98.7%; Score 1086; DB 6; Length 382;

Best Local Similarity 96.2%; Pred. No. 3.7e-102; Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISE 52
 Db 25 RLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISE 84
 QY 53 DEQKLEKFIENLLPSDGFWIGLRRREEKOSNSTACODLYANTDGSISQFRNMYVDEPS 112
 Db 85 DEQKLEKFIENLLPSDGFWIGLRRREEKOSNSTACODLYANTDGSISQFRNMYVDEPS 144

QY 113 CGSEVVMYHQPSPAGIGGYPYFQWDDRCNMKNFICKYSDKPAVPSRAEGRETE 172
DB 145 CGSEVVMYHQPSPAGIGGYPYFQWDDRCNMKNFICKYSDKPAVPSRAEGRETE 204
QY 173 LTPVLPBETQEDAKTFKESREALNLAY 203
DB 205 LTPVLPBETQEDAKTFKESREALNLAY 235

RESULT 17
ABR66146
ID ABR66146 standard; protein; 382 AA.
AC ABR66146;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO234, SEQ ID NO:20.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnetary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027278-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176987.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
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PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 11-DEC-1997; 97US-0066772P.
PR 12-DEC-1997; 97US-0069335P.
PR 17-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
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PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
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PR 31-MAR-1998; 98US-0080194P.
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PR 18-JUN-1998; 98US-0089908P.
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PR 26-JUN-1998; 98US-0090863P.

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PR	02-JUL-1998;	98US-0091486P.	Db	85	DEQKLEKFIENLLPSDGDGFWGLRRREKQSNSTACODLVAWTDGSIQFRNWWVDEPS	144
PR	02-JUL-1998;	98US-0091626P.				
PR	02-JUL-1998;	98US-0091628P.	Qy	113	CGSEVCVMYHQPSPAGIGGYPWFQWDDRCNMKNFICKYSDEKPAVPSREARGEETE	172
PR	02-JUL-1998;	98US-0091632P.				
PR	24-JUL-1998;	98US-0094006P.	Db	145	CGSEVCVMYHQPSPAGIGGYPWFQWDDRCNMKNFICKYSDEKPAVPSREARGEETE	204
PR	04-AUG-1998;	98US-0095284P.				
PR	10-AUG-1998;	98US-0095998P.	Qy	173	LTPVLPPESTOEDAKTKFKESREALNLAY	203
PR	10-AUG-1998;	98US-0096012P.				
PR	17-AUG-1998;	98US-0096757P.	Db	205	LTPVLPPESTOEDAKTKFKESREALNLAY	235
PR	17-AUG-1998;	98US-0096867P.				
PR	17-AUG-1998;	98US-0096891P.				
PR	17-AUG-1998;	98US-0096897P.				
PR	18-AUG-1998;	98US-0096949P.				
PR	18-AUG-1998;	98US-0096959P.				
PR	18-AUG-1998;	98US-0097022P.				
PR	26-AUG-1998;	98US-0097552P.				
PR	26-AUG-1998;	98US-0097954P.				
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PR	26-AUG-1998;	98US-0097971P.				
PR	26-AUG-1998;	98US-0097974P.				
PR	26-AUG-1998;	98US-0098014P.				
PR	01-SEP-1998;	98US-0098716P.				
PR	01-SEP-1998;	98US-0098723P.				
PR	02-SEP-1998;	98US-0098803P.				
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PR	24-SEP-1998;	98US-0101739P.				
PR	24-SEP-1998;	98US-0101743P.				
PR	24-SEP-1998;	98US-0101922P.				
PR	25-SEP-1998;	98US-0101786P.				
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PR	29-SEP-1998;	98US-0102331P.				
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Query Match 98.7%; Score 1086; DB 6; Length 382;

Best Local Similarity 96.2%; Pred. No. 3.7e-102;

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PR	21-APR-1998;	98US-0082569P.	PR	26-JUN-1998;	98US-0091010P.
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PR	29-APR-1998;	98US-0083496P.	PR	02-JUL-1998;	98US-0091626P.
PR	29-APR-1998;	98US-0083499P.	PR	02-JUL-1998;	98US-0091628P.
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PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100919P.
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Query Match 98.7%; Score 1086; DB 6; Length 382;

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QY 53 DEQLIEKFIENLLPSDGFWIGLRREBKQNSSTACQDLYAWTDGSIQFRNYYVDPS 112
DB 85 DEQLIEKFIENLLPSDGFWIGLRREBKQNSSTACQDLYAWTDGSIQFRNYYVDPS 144
QY 113 CGSEVCVMYHOPSPAGIGGYPMPQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 172
DB 145 CGSEVCVMYHOPSPAGIGGYPMPQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 204
QY 173 LTTPLPEETQEDAKTKFKESREAAALNAY 203
DB 205 LTTPLPEETQEDAKTKFKESREAAALNAY 235
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XX DT 27-JUN-2003 (first entry)
XX DE Human PRO polypeptide #10.
XX KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
XX KW chromosome mapping; Gene mapping; cytostatic.
XX OS Homo sapiens.
XX PN US2003032113-A1.
XX PD 13-FEB-2003.
XX PF 20-JUN-2002; 2002US-00176911.
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Best Local Similarity 96.2%; Pred. No. 3.7e-102;
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XX 10-JUN-2003 (first entry)
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XX Human; secreted and transmembrane protein; PRO polypeptide; cancer;
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PR	24-OCT-1997;	97US-0063127P.	PT	PRO1868, useful in molecular biology, chromosome and gene mapping, in
PR	24-OCT-1997;	97US-0063128P.	PT	generating antisense RNA and DNA, and in gene therapy.
PR	27-OCT-1997;	97US-0063327P.	XX	Claim 12; Fig 50; 474pp; English.
PR	27-OCT-1997;	97US-0063329P.	XX	The present invention relates to the isolation of novel human secreted
PR	28-OCT-1997;	97US-0063541P.	XX	and transmembrane proteins (PRO polypeptides), and the polynucleotide
PR	28-OCT-1997;	97US-0063542P.	CC	sequences encoding them. The polynucleotide sequences are useful in
PR	28-OCT-1997;	97US-0063544P.	CC	molecular biology, as hybridisation probes, in chromosome and gene
PR	28-OCT-1997;	97US-0063550P.	CC	mapping, in generating antisense RNA and DNA, and in gene therapy. The
PR	28-OCT-1997;	97US-0063564P.	CC	polynucleotide sequences may also be used in preparing PRO polypeptides
PR	29-OCT-1997;	97US-0063438P.	CC	by recombinant techniques, and in generating either transgenic animals or
PR	29-OCT-1997;	97US-0063704P.	CC	knock-out animals which, in turn, are useful in the development and
PR	29-OCT-1997;	97US-0063705P.	CC	screening of therapeutically useful reagents. The PRO polypeptides or
PR	29-OCT-1997;	97US-0063733P.	CC	their antibodies are useful in preparing a medicament for treating a
PR	29-OCT-1997;	97US-0064215P.	CC	condition responsive to the polypeptide or antibody, such as cancer,
PR	31-OCT-1997;	97US-0063870P.	CC	Alzheimer's disease or ischaemia, and in various diagnostic assays.
PR	31-OCT-1997;	97US-0064103P.	CC	ABU71445-ABU71505 represent human PRO polypeptides of the invention
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PR	28-JUL-2000;	2000WO-US020710.		
PR	24-AUG-2000;	2000WO-US023328.		
PR	18-SEP-2000;	2000WO-US0665350.		
XX				
PA	(GETH) GENENTECH INC.			
XX				
PI	Ashkenazi A, Bozstein D, Desnoyers L, Eaton DL, Ferrara N;			
PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;			
PI	Godowski PU, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;			
PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;			
PI	Williams PM, Wood WI;			
XX	WPI; 2003-361832/34.			

RESULT 23

ABR68085
ID ABR68085 standard; protein; 382 AA.

XX ABR68085;

XX AC
DT 11-AUG-2003 (first entry)

XX DE Human secreted polypeptide PRO234, SEQ ID NO:20.

XX Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumor necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumor; diagnosis;
KW adrenal tumor; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.

XX OS Homo sapiens.

XX PN US2003027264-A1.

XX PD 06-FEB-2003.

XX PF 18-JUN-2002; 2002US-00174579.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

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Db	85	DEQKLEKFIENLPSDGFWIGLRRREKOSNSTACODLYAWTDGSIQPRNMYVDEPS	144
QY	113	CGSECVVMYHQPAPAGIGGPFQWMDRCKNNKFNICKYDEKPAVPSREAEGBETE	172
Db	145	CGSECVVMYHQPAPAGIGGPFQWMDRCKNNKFNICKYDEKPAVPSREAEGBETE	204
QY	173	LTTPVLPSTQEDAKTFKESREANLAY	203
Db	205	LTTPVLPSTQEDAKTFKESREANLAY	235

RESULT 24	
ABU96138	ABU96138 standard; protein; 382 AA.
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DT	25-JUL-2003 (first entry)
XX	
DE	Novel human secreted and transmembrane protein PRO234.
XX	
KW	Human; secreted and transmembrane protein; PRO; transgenic animal;
KW	knockout; chromosome identification; tissue typing; tumour;
KW	chondrocyte proliferation; chondrocyte differentiation;
KW	tumor necrosis factor-alpha release stimulator.
XX	
OS	Homo sapiens.
XX	
FN	US2003036144-A1.
XX	
PD	20-FEB-2003.
XX	
PF	01-JUL-2002; 2002US-00187601.
XX	

PD 20-FEB-2003.
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Qy 53 DEQKLIKFENLLPSDGFWIGLRREKOSNSTACODLYAWTDGSIQFRNYYVDEPS 112
Db |||||
85 DEQKLIKFENLLPSDGFWIGLRREKOSNSTACODLYAWTDGSIQFRNYYVDEPS 144
Qy 113 CGSEVCVVMYHQPSPAGIGPYFMQWDDRCNMKNPFICKYSDKPAVPSREAEGETE 172
Db |||||
145 CGSEVCVVMYHQPSPAGIGPYFMQWDDRCNMKNPFICKYSDKPAVPSREAEGETE 204
Qy 173 LTTVPVLPETQEDAKTKFKESREAAALNLAY 203
Db |||||
205 LTTVPVLPETQEDAKTKFKESREAAALNLAY 235
```

Search completed: September 9, 2004, 22:53:36
Job time : 86.2899 secs

Q8c4f8 mus musculu
Q8x4q8 mus musculu
Q8c979 mus musculu
Q9xyx3 hydra magni
Q8vif6 mus musculu
Q8cj86 mus musculu
Q8bhk7 mus musculu
Q8tzw4 mus musculu
Q8d8v4 mus musculu
Q9lzx0 mus musculu
Q90wi7 burgarus fa
Q90wi7 burgarus fa
Q8cj91 mus musculu
Q95244 sus scrofa
Q8bgz0 mus musculu
Q8cj94 mus musculu
Q8cj93 mus musculu
Q8cj88 mus musculu
Q7tma7 mus musculu
Q7tsq9 mus musculu
Q7tsq7 mus musculu
Q7tsq0 mus musculu
Q7tsq1 mus musculu
Q90wm2 xenopus lae
Q8cj89 mus musculu
Q8cj92 mus musculu
Q725k9 homo sapien
Q95lq3 odocoileus
Q90wif burgarus mu
Q8ixk1 homo sapien

17 169 15.4 217 11 Q8C4F8
18 165.5 15.0 742 11 Q8X4Q8
19 165.5 15.0 742 11 Q8C979
20 161.5 14.7 134 5 Q9XYX3
21 159.5 14.5 742 11 Q8VIF6
22 158 14.4 142 11 Q8CJ86
23 158 14.4 142 11 Q8BHK7
24 158 14.4 295 11 Q9LZXW4
25 158 14.4 311 11 Q9D8V4
26 158 14.4 325 11 Q9LZX0
27 157 14.3 158 13 Q90WI7
28 156 14.2 323 11 Q8CJ91
29 156 14.2 339 6 Q95244
30 155 14.1 293 11 Q8BGZ0
31 155 14.1 323 11 Q8CJ94
32 155 14.1 323 11 Q8CJ93
33 155 14.1 323 11 Q8CJ88
34 155 14.1 379 11 Q7TMA7
35 155 14.1 473 11 Q7TSP9
36 155 14.1 477 11 Q7TSP7
37 155 14.1 504 11 Q7TSQ0
38 155 14.1 534 11 Q7TSQ1
39 155 14.1 1152 13 Q90WM2
40 154 14.0 322 11 Q8CJ89
41 154 14.0 323 11 Q8CJ92
42 153 13.9 446 4 Q725K9
43 152.5 13.9 485 6 Q95LG3
44 152 13.8 158 13 Q90WI6
45 151.5 13.8 652 4 Q8IXK1

ALIGNMENTS

RESULT 1

Q8TAY8 PRELIMINARY; PRT; 374 AA.
ID Q8TAY8
AC Q8TAY8; 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Similar to unnamed protein product.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC025407; A425407.1; -
DR GO: GO:0005529; F-sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C TYPE LECTIN_2; 1.
SQ SEQUENCE 374 AA; 42312 MW; FC214E6BC9B578D9 CRC64;

Query Match 100.0%; Score 1100; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.2e-97;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKACRRDGGQLVSISEDEQKLIK 60
DB 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKACRRDGGQLVSISEDEQKLIK 84
QY 61 FIENLLSDGDFWGLRRREKQSNSTACODLVAWTDGSIQFRNWTVDSPSCSEVCVV 120
DB 85 FIENLLSDGDFWGLRRREKQSNSTACODLVAWTDGSIQFRNWTVDSPSCSEVCVV 144
QY 121 MYHOPSAPAGTGGPYMFQWDDRCNMKNFICKYSDKPAVPGRAREGETELTPVLPE 180
|||

OM protein - protein search, using sw model

Run on: September 9, 2004, 22:47:24 ; Search time 71.8231 Seconds
(without alignments)
891.777 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227

Perfect score: 1100

Sequence: 1 RLLSGQPVCRGGTQPCYK.....EEDAKTKFESREALNLAY 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertibrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	100.0	374	Q8TAY8	Q8tay8 homo sapien
2	1100	100.0	374	Q9GNF3	Q9gnf3 homo sapien
3	1096	99.6	374	Q96NC5	Q96nc5 homo sapien
4	939.5	85.4	374	Q92209	Q92209 cricetus
5	797.5	72.5	211	Q8C351	Q8c351 mus musculu
6	580	52.7	246	Q8BM17	Q8bmi7 mus musculu
7	580	52.7	292	Q8BVU2	Q8bvui2 mus musculu
8	513	46.6	236	Q7Z798	Q7z798 homo sapien
9	504.5	45.9	232	Q7Z799	Q7z799 homo sapien
10	500	45.5	236	Q7Z7A0	Q7z7a0 homo sapien
11	185	16.8	1290	Q9W6E1	Q9w6e1 gallus gall
12	178.5	16.2	1456	Q11830	Q11830 mus musculu
13	177.5	16.1	1348	Q25199	Q25199 hydra atten
14	176.5	16.0	1479	Q9V5P9	Q9v5p9 homo sapien
15	176.5	16.0	1479	Q9UBG0	Q9ubg0 homo sapien
16	170.5	15.5	1479	Q64449	Q64449 mus musculu

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Db 145 MYHQPAPAGIGPYFMFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTPVLPE 204
QY 181 ETQEDAKTKFKESREAAINLAY 203
Db 205 ETQEDAKTKFKESREAAINLAY 227

RESULT 2
Q96NF3 ID Q96NF3 PRELIMINARY; PRT; 374 AA.
AC Q96NF3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical protein FLJ30977.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hata T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Chiba Y.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RA "NEO human cDNA sequencing project.";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK055539; BAB70946.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C.TYPE_LECTIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 374 AA; 42280 MW; 8AE64E6BC9B56DCD CRC64;

Query Match 100.0%; Score 1100; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.2e-97;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQLVSISEDEQKLIK 60
Db 25 RLLSQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQLVSISEDEQKLIK 84
QY 61 FIENLLPSDGFWIGLRREKQNSACQDIYAWTDGSIQFRNWWYDPPSCGSEVCV 120
Db 85 FIENLLPSDGFWIGLRREKQNSACQDIYAWTDGSIQFRNWWYDPPSCGSEVCV 144
QY 121 MYHQPAPAGIGPYFMFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTPVLPE 180
Db 145 MYHQPAPAGIGPYFMFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTPVLPE 204
QY 181 ETQEDAKTKFKESREAAINLAY 203
Db 205 ETQEDAKTKFKESREAAINLAY 227

RESULT 3
Q96NC5 ID Q96NC5 PRELIMINARY; PRT; 374 AA.
AC Q96NC5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical protein FLJ31092.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Borowsky M.L., Hynes R.O.;
RA "Laylin, a novel talin-binding transmembrane protein homologous with
RA C-type lectins, is localized in membrane ruffles.";
RL J. Cell Biol. 143:0-0(1998).
DR EMBL; AF093673; AAC68695.1; -.
DR HSSP; P22897; LEGG.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C.TYPE_LECTIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 374 AA; 42435 MW; 298A8BA24FB04E1C CRC64;

Query Match 85.4%; Score 939.5; DB 11; Length 374;
Best Local Similarity 85.8%; Pred. No. 3.5e-82;

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RN [1]
RP SEQUENCE FROM N.A.
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K.,
RA Isogai T.;
RA "NEO human cDNA sequencing project.";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK055654; BAB70978.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C.TYPE_LECTIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 374 AA; 42310 MW; CBF74E676E23BA16 CRC64;

Query Match 99.6%; Score 1096; DB 4; Length 374;
Best Local Similarity 99.5%; Pred. No. 2.9e-97;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLLSQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQLVSISEDEQKLIK 60
Db 25 RLLSQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQLVSISEDEQKLIK 84
QY 61 FIENLLPSDGFWIGLRREKQNSACQDIYAWTDGSIQFRNWWYDPPSCGSEVCV 120
Db 85 FIENLLPSDGFWIGLRREKQNSACQDIYAWTDGSIQFRNWWYDPPSCGSEVCV 144
QY 121 MYHQPAPAGIGPYFMFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTPVLPE 180
Db 145 MYHQPAPAGIGPYFMFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTPVLPE 204
QY 181 ETQEDAKTKFKESREAAINLAY 203
Db 205 ETQEDAKTKFKESREAAINLAY 227

RESULT 4
Q92209 ID Q92209 PRELIMINARY; PRT; 374 AA.
AC Q92209;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Laylin.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Borowsky M.L., Hynes R.O.;
RA "Laylin, a novel talin-binding transmembrane protein homologous with
RA C-type lectins, is localized in membrane ruffles.";
RL J. Cell Biol. 143:0-0(1998).
DR EMBL; AF093673; AAC68695.1; -.
DR HSSP; P22897; LEGG.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C.TYPE_LECTIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 374 AA; 42435 MW; 298A8BA24FB04E1C CRC64;

Query Match 85.4%; Score 939.5; DB 11; Length 374;
Best Local Similarity 85.8%; Pred. No. 3.5e-82;

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Qy 1 RLLSQPVCRGGTQPCVKVIYFHTSRLNFEAKACRRDGGQLVSISEDEQKLIK 60
Db 25 RLLSQPVCRGGTQPCVKVIYFHTSRLNFEAKACRRDGGQLVSIETEDQRLIK 84
Qy 61 FIENLLSDGDFWIGLRREKQSNSTACQDLYAWTDGSIQSRNWNVYDEPSCGVCVV 120
Db 85 FIENLLASDGDGFWIGLRLEVKQNVNACQDLYAWTDGSIQSRNWNVYDEPSCGVCVV 144
Qy 121 MYHQSAPAGIGGPFQWMDRRCNMKNFICKYSDEKPA-VPSREAGESETLTTPVLP 179
Db 145 MYHQSAPAGIGGPFQWMDRRCNMKNFICKYADEKPSPTTSIRPGGEATEPPTPVL 204
Qy 180 BETOEEDAKTFKESRAALNLAY 203
Db 205 BETOEEDAKTFKESRAALNLAY 228

RESULT 5
Q8C351 PRELIMINARY; PRT; 211 AA.
ID Q8C351;
AC Q8C351;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE LAYLIN homolog (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK086930; BAC39765.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C TYPE LECTIN_2; 1.
FT NON_TER 211
FT SEQUENCE 211 AA; 23697 MW; AD9870B5957DD5AE CRC64;

Query Match 72.5%; Score 797.5; DB 11; Length 211;
Best Local Similarity 79.7%; Pred. No. 8.4e-69;
Matches 149; Conservative 9; Mismatches 20; Indels 9; Gaps 2;

Qy 1 RLLS-----GQPVCRGGTQPCVKVIYFHTSRLNFEAKACRRDGGQLVSISE 52
Db 25 RLLSASDLDPRGQLVCRGGTQPCVKVIYFHTSRLNFEAKACRRDGGQLVSIET 84
Qy 53 DEQKLIKFIENLLSDGDFWIGLRREKQSNSTACQDLYAWTDGSIQSRNWNVDEPS 112
Db 85 DEQRLJEKFIENLLASDGDGFWIGLRLEKLEBKQSNNTACQDLYAWTDGSIQSRNWNVDEPS 144
Qy 113 CGSEVCVMYHQSAPAGIGGPFQWMDRRCNMKNFICKYSDEKPA-VPSREAGESET 171
Db 145 CGSEVCVMYHQSAPAGIGGPFQWMDRRCNMKNFICKYADEKPSPTTSIRPGGEAT 204
Qy 172 ELTTPVL 178
Db 205 EPTAPLL 211

RESULT 6
Q8BM17 PRELIMINARY; PRT; 246 AA.
ID Q8BM17
AC Q8BM17;
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DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE C-type lectin protein MT75 homolog.
GN CHODL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK031063; BAC27234.1; -.
DR MGD; MGI:2179069; Chodl.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C TYPE LECTIN_2; 1.
SQ SEQUENCE 246 AA; 27394 MW; E872660C58267752 CRC64;

Query Match 52.7%; Score 580; DB 11; Length 246;
Best Local Similarity 57.9%; Pred. No. 9.3e-48;
Matches 110; Conservative 26; Mismatches 40; Indels 14; Gaps 5;

Qy 1 RLLSQPVCRGGTQPCVKVIYFHTSRLNFEAKACRRDGGQLVSISEDEQKLIK 60
Db 23 RVVSGQKVCFADVKHPCYKXAYFHELSRVSFQEARLACESEGGVLLSLENAEQKLIES 82
Qy 61 FIENLLP-----SDGDFWIGLRREKQSNSTACQDLYAWTDGSIQSRNWNVYDEPSCGS 115
Db 83 MLQNLKTPGTGIGDGFWIGLRSGDGTQ-SGACPDLYQWSDGSSSQFRNWNVYDEPSCGS 141
Qy 116 EVCVMYHQSAPAGIGGPFQWMDRRCNMKNFICKYSDE-KPAVPSREAGESETLT 174
Db 142 EKCVMYHQSAPAGIGGPFQWMDRRCNMKNFICKYFEIHPTEPA-----EKPYLT 196
Qy 175 TPVLPETQE 184
Db 197 NQ--PEETHE 204

RESULT 7
Q8BVU2 PRELIMINARY; PRT; 292 AA.
ID Q8BVU2
AC Q8BVU2;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE C-type lectin protein MT75 homolog.
GN CHODL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK076523; BAC36378.1; -.
DR MGD; MGI:2179069; Chodl.
DR GO; GO:0005529; F:sugar binding; IEA.
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[illegible]

RESULT 11					
QW6E1	PRELIMINARY;	PRT; 1290 AA.			
ID	Q9WGE1				
AC	Q9WGE1				
DT	01-NOV-1999 (TREMBLrel. 12, Created)				
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE	Neurocan core protein.				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20309833; PubMed=10851024;				
RA	Li H., Leung T.C., Hoffman S., Balsamo J., Lillien J.;				
RT	"Coordinate Regulation of Cadherin and Integrin Function by the				
RT	Chondroitin Sulfate Proteoglycan Neurocan.";				
RL	J. Cell Biol. 149:1275-1288(2000).				
DR	EMBL; AF116856; AAD24546.2; -.				
DR	HSP; P08709; IBF9.				
DR	GO; GO:0005509; F.calcium ion binding; IEA.				
DR	GO; GO:0005540; F.hyaluronic acid binding; IEA.				
DR	GO; GO:0005529; F.sugar binding; IEA.				
DR	GO; GO:0007155; P.cell adhesion; IEA.				
DR	InterPro; IPR000152; ASx hydroxyl_S.				
DR	InterPro; IPR000742; EGF_2.				
DR	InterPro; IPR001881; EGF_Ca.				
DR	InterPro; IPR001438; EGF_I.				
DR	InterPro; IPR006209; EGF_like.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR001304; Lectin_C.				
DR	InterPro; IPR000538; Link.				
DR	InterPro; IPR000436; Sushi_SCR_CCP.				
DR	Pfam; PF00008; EGF; 2.				
DR	Pfam; PF00047; ig; 1.				
DR	Pfam; PF00059; lectin_c; 1.				
DR	Pfam; PF00084; sushi; 1.				
DR	Pfam; PF00193; Xlink; 2.				
DR	PRINTS; PR00010; EGF_BLOOD.				
DR	PRINTS; PR01265; LINKMODULE.				
DR	ProDom; PD000918; Link; 2.				
DR	SMART; SM00032; CCP; 1.				
DR	SMART; SM00034; CLECT; 1.				
DR	SMART; SM00179; EGF_CA; 1.				
DR	SMART; SM00409; IG; 1.				
DR	SMART; SM00445; LINK; 2.				
DR	PROSITE; PS00010; ASX HYDROXYL; 1.				
DR	PROSITE; PS00615; C_TYPE_LECTIN_1; 1.				
DR	PROSITE; PS00041; C_TYPE_LECTIN_2; 1.				
DR	PROSITE; PS00022; EGF_1; 2.				
DR	PROSITE; PS01186; EGF_2; 1.				
DR	PROSITE; PS01187; EGF_CA; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
DR	PROSITE; PS01241; LINK; 2.				
KW	EGF-like domain.				
SQ	SEQUENCE 1290 AA; 138877 MW; 182BD86D0E40BE78 CRC64;				
Query Match 16.8%; Score 185; DS 13; Length 1290;					
Best Local Similarity 34.7%; Pred.No. 8.le-09;					
Matches 50; Conservative 18; Mismatches 42; Indels 34; Gaps :					
QY	14 QRCYKVIYTHDTSRLNFPEAKEACHRDGQLVSTSEDEFQKLIEKFENILPDSGDWF 73	:	:	:	:
Db	1064 QGHCYR--YP---SRRSWEDAERDCRRAGHLTSHSQEHGFINSF-----GHENTW 1112	:	:	:	:
QY	74 IGLRRREEKSGNSTACDLVAWTDGISTSQFNWVVDPS---CGSEVCVVWY-HQPSAPA 129	:	:	:	:
Db	1113 IGLNDRIVEDQ-----FQWDNTGLQYENRFENQPDNFFAGGEDCVLVSHSHE----- 1159	:	:	:	:

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Db 866 ISMDKK-----FIWMDGSKVDFVATGEPNFANDENCVTMY-----TNSGF----- 908
QY 136 MFQWDDRCNMKNFICK---YSDEKPAVPSPREASGEETELTTPVLPRETOB----- 184
Db 909 ---WINDINGCYFNFCIQHNSINATAMP-----TTPTPGCKEGWHLYKNK 954
QY 185 -----EDAKTKFKESREALNL 201
Db 955 CFKIFGFANEKXKQWDAQACKGL 979

RESULT 13
Q25199 PRELIMINARY; PRT; 1348 AA.
AC Q25199;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tyrosine kinase receptor.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Irvine;
RX MEDLINE=20209407; PubMed=10744720;
RA Reidling J.C., Miller M.A., Steele R.E.;
RT "Sweet Tooth, a Novel Receptor Protein-Tyrosine Kinase with C-type
RT Lactin-like Extracellular Domains.";
RL J. Biol. Chem. 275:10323-10330(2000).
DR EMBL; J22612; AA29218.2; -.
DR HSSP; F11362; IFCK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001304; Lactin_C.
DR InterPro; IPR003990; P:creatase.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00059; lectin_c_4.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR01504; PNCREATITAP.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00034; CLECT; 4.
DR SMART; SM00219; TyRc; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 2.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 1348 AA; 156916 MW; 77D2122093227FEF CRC64;

Query Match 16.1%; Score 177.5; DB 5; Length 1348;
Best Local Similarity 28.0%; Pred. No. 4.5e-08;
Matches 47; Conservative 32; Mismatches 46; Indels 43; Gaps 8;

QY 3 LSGQFVC---RGGTQPC-----YKVIYFHDTSRLNFEAKEACRRDGGQLVSISEDE 54
Db 412 LSHRFICKVKRATNEYCAEGWTSYRIVCYFIYSIEFDWFKSFSSCQIGNLLSIENQEE 471
QY 55 QKLEKFTENLLPSDGD-FWIGLR-----REKQSNSTACQDLYAWTDCGISQFRNWTY 107
Db 472 ---NRFTENGLIKNDKYGLNKNWYDLKKYK-----FEWSDNTYQFPNWI 518
QY 108 VDEP---SCGSEVVCVMVHQPSAPAGIGGPFYQWDDRCNMKNFNICK 153
Db 519 TNQPDNNGIIBSCVMYNY-----GWSDECKVLNGFICK 553

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RESULT 14
Q9Y5P9 PRELIMINARY; PRT; 1479 AA.
AC Q9Y5P9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Endocytic receptor Endo180.
GN ENDO180.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20148849; PubMed=10683150;
RA Sheikh H., Yarwood H., Ashworth A., Isacke C.;
RT "Endo180, an endocytic recycling glycoprotein related to the
RT macrophage mannose receptor is expressed on fibroblasts, endothelial
RT cells and macrophages and functions as a lectin receptor.";
RL J. Cell Sci. 113:1021-1032(2000).
DR EMBL; AFL34838; AAD30280.1; -.
DR HSSP; P02751; 2PN2.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005215; P:transport activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lactin_C.
DR InterPro; IPR000566; Lipocin_cycPAPP.
DR InterPro; IPR008997; RicinB_lectin.
DR InterPro; IPR000772; RicinB_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c_8.
DR PRINTS; PR00013; ENTVEPII.
DR ProDom; PD000395; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 3.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS00231; RICIN_B_LECTIN; 1.
KW Receptor.
SQ SEQUENCE 1479 AA; 166669 MW; 9F4BAF355F036FCE CRC64;

Query Match 16.0%; Score 176.5; DB 4; Length 1479;
Best Local Similarity 30.4%; Pred. No. 6.3e-08;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;

QY 4 SQQVCRGCTQPCYKVIYFHDTSRLNFEAKEACRRDGGQLVSISEDEQKLEKIE 63
Db 385 SQQPF-----QGHCVRL-----QAEKRSWQSKKACLRGGDLVSIHSMAELEFTKQIK 434
QY 64 NLLPSDGDWFGLRRRREKQSNSTACQDLYAWTDCGISQFRNWTYDEPS---CGSEVCVV 120
Db 435 QEVE---ELWIGL-----NDLKLQNFWSQGLSVSFTHWHPFENFRDLSLEDCVT 483
QY 121 MYHQPSAPAGIGGPFYQWDDRCNMKNFNICKYSDKPAVPSPREAG 168
Db 484 IW---GPEG-----RWNDSPCNQSLPSICKKAGQLSQGAABEDHG 520

RESULT 15
Q9UBG0 PRELIMINARY; PRT; 1479 AA.
AC Q9UBG0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

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DR Urokinase receptor-associated protein UPARAP.
GN KIAA0709
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Behrendt N., Jensen O.N., Engelholm L.H., Mortz E., Mann M., Dano K.;
RT "A urokinase receptor-associated protein with specific collagen-
RL binding properties."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nomura N., Chara O.;
RC TISSUE=Brain;
EX MEDLINE=98403880; PubMed=9734911;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
EL code for large proteins in vitro."
EL DNA Res. 5:159-176(1998).
DR EMBL; AF107292; AAF14132.1; -
DR EMBL; AB014609; BAA31684.1; -
DR HSSP; P02751; 2FN2.
DR Genew; HGNC:16875; MRC2.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005215; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR008997; RicinB_Like.
DR InterPro; IPR000772; Ricin_E_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c; 8.
DR PRINTS; PR00036; ANTIFREEZEII.
DR PRINTS; PR00013; FNTYPEII.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 3.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS0231; RICIN_B_LLECTIN; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1479 AA; 166654 MW; C7593EA78E2792D1 CRC64;

Query Match 16.0%; Score 176.5; DB 4; Length 1479;
Best Local Similarity 30.4%; Pred. No. 6.3e-08;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;

QY 4 SQPVCRCGGTQPCVKYVYFHDTSRLNPFEEAKACRRDGGQLVSTESDEOKLIEKFIE 63
Db 385 SQPP-----QHCYRL-----QAEKRWQSKKACLRGGDLVSIHSMAELEFITKQIK 434
QY 64 NLLPSDGDFTWIGLRREERKQSNSTACQDLYAWTDGSIQFRNMYVDPPS---CGSEYCVV 120
Db 435 QEVE---ELWIGL-----NDLKLQNFWSGSLVSFTWHFPPNNFRDSDLEDCVT 483

QY 121 MYQPSAPAGIGGPPYMFQWDDRCNMKNFKICK 168
Db 484 IW-----GPEG-----RWNDSPCQSLPSICKKAGQLSQGAABEDHG 520

RESULT 16
Q64449
ID Q64449
AC Q64449;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match 15.5%; Score 170.5; DB 11; Length 1479;
Best Local Similarity 31.4%; Pred. No. 2.4e-07;
Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;

QY 4 SQPVCRCGGTQPCVKYVYFHDTSRLNPFEEAKACRRDGGQLVSTESDEOKLIEKFIE 63
Db 384 SQPP-----QHCYRL-----QAEKRWQSKKACLRGGDLVSIHSMAELEFITKQIK 433
QY 64 NLLPSDGDFTWIGLRREERKQSNSTACQDLYAWTDGSIQFRNMYVDPPS---CGSEYCVV 120
Db 434 QEVE---ELWIGL-----NDLKLQNFWSGSLVSFTWHFPPNNFRDSDLEDCVT 482

QY 121 MYQPSAPAGIGGPPYMFQWDDRCNMKNFKICK 153
Db 483 IW-----GPEG-----RWNDSPCQSLPSICK 504

RESULT 17
Q8C4F8
ID Q8C4F8
AC Q8C4F8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chondroitin sulfate proteoglycan 3 (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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[illegible]

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QY 82 KOSNSTACODLYAWTDGSI--SQFRN-WYVDEP-SCGSEVCVMVYHOPSAPAGIGGPFYMF 137
Db 79 EAT-----WLWVDGSLSRQKYNRGEPNNGEEDCVP-----AGDG----- 118

QY 138 QWDDRCNMKNFICKYSDKPAVPSRE 165
Db 119 -WNSKCEKELKWLCK-----KSATPCTE 141

RESULT 23
Q8BHK7 PRELIMINARY; PRT; 142 AA.
AC Q8BHK7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SIGNR1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Park C.G., Steinman R.M.;
RT "Alternatively Spliced Forms of Mouse DC-SIGN Homologs.";
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL AF374471; AAL27540.1; -
DR MGD; MGI:1916415; CG209b.
DR GO:GO:005529; F.sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C.TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C.TYPE_LECTIN_2; 1.
SQ SEQUENCE 295 AA; 3388 MW; A491F7D3551A91D0 CRC64;

Query Match 14.4%; Score 158; DB 11; Length 295;
Best Local Similarity 32.4%; Pred. No. 5.5e-07;
Matches 48; Conservative 21; Mismatches 45; Indels 34; Gaps 9;

QY 22 YFHTSRLNPFEEAKCRDGGQGVSTESDEQKLEKFIENLLPSDGDWIGLRREE 81
Db 177 YFFSKSR-NWMDAVTACKVEKVAQLVINSDDEQ-----TFLQOTS KAKGTWGLSLDKK 231

QY 82 KOSNSTACODLYAWTDGSI--SQFRN-WYVDEP-SCGSEVCVMVYHOPSAPAGIGGPFYMF 137
Db 232 EAT-----WLWVDGSLSRQKYNRGEPNNGEEDCVP-----AGDG----- 271

QY 138 QWDDRCNMKNFICKYSDKPAVPSRE 165
Db 272 -WNSKCEKELKWLCK-----KSATPCTE 294

RESULT 25
Q8BHK7 PRELIMINARY; PRT; 311 AA.
AC Q8BHK7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1810030122Bik protein.
GN CD209B OR 1810030122Bik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pancreas;
RX MEDLINE=21085860; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner T., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide T., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

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QY 82 KOSNSTACODLYAWTDGSI--SQFRN-WYVDEP-SCGSEVCVMVYHOPSAPAGIGGPFYMF 137
Db 79 EAT-----WLWVDGSLSRQKYNRGEPNNGEEDCVP-----AGDG----- 118

QY 138 QWDDRCNMKNFICKYSDKPAVPSRE 165
Db 119 -WNSKCEKELKWLCK-----KSATPCTE 141

RESULT 23
Q8BHK7 PRELIMINARY; PRT; 142 AA.
AC Q8BHK7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SIGNR1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Spleen;
RX MEDLINE=22133304; PubMed=12137941;
RA Parent S.A., Zhang T., Chretien G., Clemas J.A., Figueroa D.J., Ky B.,
RA Blevins R.A., Austin C.P., Rosen H.;
RT "Molecular characterization of the murine SIGNR1 gene encoding a C-
type lectin homologous to human DC-SIGN and DC-SIGNR.";
RL Gene 233:33-46(2002).
DR EMBL; AF424800; AAN75595.1; -
DR EMBL; AF424801; AAN75596.1; -
DR GO:GO:0005529; F.sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C.TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C.TYPE_LECTIN_2; 1.
FT NON TER 1
SQ SEQUENCE 142 AA; 16471 MW; OCB363A383D887EF CRC64;

Query Match 14.4%; Score 158; DB 11; Length 142;
Best Local Similarity 32.4%; Pred. No. 2.3e-07;
Matches 48; Conservative 21; Mismatches 45; Indels 34; Gaps 9;

QY 22 YFHTSRLNPFEEAKCRDGGQGVSTESDEQKLEKFIENLLPSDGDWIGLRREE 81
Db 24 YFFSKSR-NWMDAVTACKVEKVAQLVINSDDEQ-----TFLQOTS KAKGTWGLSLDKK 78

QY 82 KOSNSTACODLYAWTDGSI--SQFRN-WYVDEP-SCGSEVCVMVYHOPSAPAGIGGPFYMF 137
Db 79 EAT-----WLWVDGSLSRQKYNRGEPNNGEEDCVP-----AGDG----- 118

QY 138 QWDDRCNMKNFICKYSDKPAVPSRE 165
Db 119 -WNSKCEKELKWLCK-----KSATPCTE 141

RESULT 24
Q91ZW4 PRELIMINARY; PRT; 295 AA.
AC Q91ZW4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SIGNR1 TM-less isoform.
GN CD209B OR SIGNR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Search completed: September 9, 2004, 22:56:42
Job time : 73.3231 secs

Blank Sheet

OM protein - protein search, using sw model

Run on: September 9, 2004, 22:46:49 ; Search time 14.9631 Seconds
(without alignments)
706.418 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227

Perfect score: 1100
Sequence: 1 RLISGQPVCRGGTQPCYKV.....BEDAKTKPESREALNLAY 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	574	52.2	273	1	CHOD_MOUSE	Q9cxb0 mus musculus
2	561.5	51.0	273	1	CHOD_HUMAN	Q9h9p2 homo sapien
3	182	16.5	1456	1	MANR_HUMAN	P22897 homo sapien
4	177	16.1	1268	1	PGCN_MOUSE	P55066 mus musculus
5	176	16.0	1321	1	PGCN_HUMAN	O14594 homo sapien
6	174.5	15.9	3381	1	PGCV_BOVIN	P81282 bos taurus
7	174	15.8	1257	1	PGCV_RAT	P55067 rattus norv
8	174	15.8	2738	1	PGCV_RAT	Q9erba rattus norv
9	174	15.8	3358	1	PGCV_MOUSE	Q62059 mus musculus
10	174	15.8	3396	1	PGCV_HUMAN	P13611 homo sapien
11	171	15.5	3562	1	PGCV_CHICK	Q90753 gallus norv
12	164	14.9	643	1	CD93_RAT	Q90761 rattus norv
13	158.5	14.4	2364	1	PGCA_BOVIN	P13608 bos taurus
14	158.5	14.4	2415	1	PGCA_HUMAN	P16112 homo sapien
15	155.5	14.1	2333	1	PGCA_CANFA	Q28343 canis fami
16	154.5	14.0	612	1	LEW2_MOUSE	Q00690 mus musculus
17	153.5	14.0	644	1	CD93_MOUSE	O89103 mus musculus
18	153.5	14.0	2124	1	PGCA_RAT	P07897 rattus norv
19	152	13.8	512	1	PGCB_BOVIN	Q28062 bos taurus
20	151.5	13.8	652	1	CD93_HUMAN	Q9np93 homo sapien
21	151	13.7	197	1	CLE1_HUMAN	P07596 homo sapien
22	149	13.5	321	1	FCB2_HUMAN	P06734 homo sapien
23	147.5	13.4	2132	1	PGCB_MOUSE	Q61282 mus musculus
24	147	13.4	883	1	PGCB_CHICK	Q61361 mus musculus
25	146	13.3	2109	1	PGCB_MOUSE	P07898 gallus norv
26	145	13.2	158	1	LEGC_TRIST	Q9ysp1 trimeresuru
27	145	13.2	883	1	PGCB_RAT	P55068 rattus norv
28	144.5	13.1	173	1	LEGC_MEGRO	P17346 megabalanus
29	144.5	13.0	372	1	LEW1_RAT	P30836 rattus norv
30	143.5	13.0	372	1	LEW1_MOUSE	P18337 mus musculus
31	141.5	12.9	331	1	FCB2_MOUSE	P20693 mus musculus
32	141.5	12.9	549	1	LEW2_RAT	P98105 rattus norv
33	140.5	12.8	162	1	LEC3_MEGRO	P07439 megabalanus

34	140	12.7	370	1	LEM1_BOVIN	P98131 bos taurus
35	139	12.6	248	1	PSPA_HUMAN	P07714 homo sapien
36	139	12.6	283	1	LECA_SARPE	P05047 sarcophaga
37	138.5	12.6	152	1	IXA_TRIFL	P23806 trimeresuru
38	138.5	12.6	202	1	LETN_MOUSE	P43025 mus musculus
39	137.5	12.5	372	1	LEM1_MACMU	Q95198 macaca mula
40	137.5	12.5	372	1	LEM1_PAPHA	Q28768 papio hamad
41	136	12.4	175	1	LITH_BOVIN	P23132 bos taurus
42	135	12.3	165	1	LITI_MOUSE	P43137 mus musculus
43	134.5	12.2	132	1	ACAL_ANSA	P83300 anser anser
44	134.5	12.2	372	1	LEM1_PONPY	Q95235 pongo pygma
45	134.5	12.2	485	1	LEM2_BOVIN	P98107 bos taurus

ALIGNMENTS

RESULT 1

CHOD_MOUSE

ID	CHOD_MOUSE	STANDARD	PRT	273 AA
AC	Q9CXB0; Q8V131;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Chondrolectin precursor (Transmembrane protein MT75).			
GN	CHODL			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J;			
RA	Wang L., Smits P., Hubner R., Wouters J., Merregaert J.;			
RT	"Mc75, a low expressed c-type lectin gene involving in			
RT	Chondrogenesis."			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DDJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Embryonic head;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukushima Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,			
RA	Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,			
RA	Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,			
RA	Hayashizaki Y.;			
RA	Functional annotation of a full-length mouse cDNA collection.;			
RT	Nature 409:685-690(2001).			
RL	- SUBCELLULAR LOCATION: Type I membrane protein (Potential).			
CC	- SIMILARITY: Contains 1 C-type lectin family domain.			
CC	- SIMILARITY: Contains 1 C-type lectin family domain.			
CC	-----			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF311699; AAL50354.1; --			

DR SMART; SM00059; FN2; 1.
 DR SMART; SM00458; RICIN; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; 6.
 DR PROSITE; PS00641; C-TYPE LECTIN 2; 8.
 DR PROSITE; PS00023; FIBRONECTIN 2; 1.
 DR PROSITE; PS00231; RICIN B LECTIN; 1.
 KW Receptor; Signal; Calcium-binding; Transmembrane; Repeat;
 KW Glycoprotein; Endocytosis; Macrophage; Lectin; Antigen; 3D-structure.
 FT SIGNAL 1 18
 FT CHAIN 19 1456
 FT DOMAIN 19 1383
 FT TRANSMEM 1384 1411
 FT DOMAIN 1412 1456
 FT DOMAIN 22 142
 FT DOMAIN 157 212
 FT DOMAIN 216 344
 FT DOMAIN 360 490
 FT DOMAIN 502 629
 FT DOMAIN 644 781
 FT DOMAIN 805 926
 FT DOMAIN 943 1083
 FT DOMAIN 1100 1216
 FT DOMAIN 1228 1359
 FT DISULFID 646 659
 FT DISULFID 680 777
 FT DISULFID 753 769
 FT CARBOHYD 104 104
 FT CARBOHYD 344 344
 FT CARBOHYD 529 529
 FT CARBOHYD 926 926
 FT CARBOHYD 930 930
 FT CARBOHYD 1160 1160
 FT CARBOHYD 1205 1205
 FT CARBOHYD 1311 1311
 FT TURN 648 649
 FT STRAND 651 652
 FT TURN 654 655
 FT STRAND 658 663
 FT HELIX 667 669
 FT STRAND 671 671
 FT HELIX 673 683
 FT TURN 684 684
 FT STRAND 686 687
 FT HELIX 693 705
 FT TURN 706 707
 FT TURN 709 710
 FT STRAND 712 718
 FT TURN 723 724
 FT STRAND 727 727
 FT TURN 729 730
 FT STRAND 733 733
 FT TURN 741 742
 FT HELIX 746 748
 FT STRAND 752 757
 FT TURN 758 761
 FT STRAND 764 768
 FT TURN 769 770
 FT STRAND 773 780
 FT TURN 781 782
 SQ SEQUENCE 1456 AA; 166011 MW; 264E5AF3C576A5E3 CRC64;

Query Match
 Best Local Similarity 16.5%; Score 182; DB 1; Length 1456;
 Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;

QY 18 YKVIYFHTSRILNFEAKACRDRGGLVSIQSEDEQKLIKFIENLLPSDGDFFIGLR 77
 DB 807 YKDYQYVFSKEKETMDNARAFCKNFGLVSIQSESEKFLWKYV-NRNDQAQAYFIGLL 865
 QY 78 RREEKQNSTACQDLXAWTDGISQFNWYVDEPSGCS--EVCVMYVHQSPAPAGIGGPY 135
 DB 866 ISLDKK-----FAWMDGSKYDVYVSWATGFNFANEDENCVTMY-----SNSGF----- 908

QY 136 MFWNDNDRCNMKNFKICKYSDK-----PAVPSREABGEETELTPVLPETOE----- 184
 DB 909 ---WNDINGCPYNAFICQRHNSINATTWMP-----TMPSPVSGCKEGNFWYSN 954
 QY 185 -----EDAKKTKESREAAAL 199
 DB 955 KCFKIFGFMEERKNWQEARAKCI 978
 RESULT 4
 PGCN MOUSE
 ID PGCN_MOUSE STANDARD; PRT; 1268 AA.
 AC PS5066;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 GN Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
 GN CSPG3 OR NCAN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=96039250; PubMed=7490074;
 RA Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
 RA Faessler R.;
 RT "Structure and chromosomal localization of the mouse neurocan gene.";
 RL Genomics 28:405-410(1995).
 CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
 CC development by binding to neural cell adhesion molecules (NG-CAM
 CC and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
 CC acid.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
 CC -----
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 CC -----
 DR EMBL; X84727; CA559216.1; -.
 DR FIR; S52781; S52781.
 DR HSP; P00740; 1EDM.
 DR MGD; MGI:104694; Cspg3.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR000152; Asx hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR000538; Link.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF00084; sushi; 1.
 DR Pfam; PF00193; Xlink; 2.
 DR PRINTS; PR00356; ANTIFREEZEII.
 DR PRINTS; PR01265; LINKMODULE.
 DR PRODOM; PD0000318; Link; 2.
 DR SMART; SM00032; CCP; 1.

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DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
KW EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
FT SIGNAL 1 22
FT CHAIN 23 1268
FT DOMAIN 37 157
FT DOMAIN 158 253
FT DOMAIN 259 355
FT DOMAIN 960 996
FT DOMAIN 998 1034
FT DOMAIN 1036 1165
FT DOMAIN 1166 1224
FT DISULFID 58 139
FT DISULFID 181 252
FT DISULFID 205 226
FT DISULFID 279 354
FT DISULFID 303 324
FT DISULFID 964 975
FT DISULFID 969 984
FT DISULFID 986 995
FT DISULFID 1040 1051
FT DISULFID 1068 1160
FT DISULFID 1136 1152
FT DISULFID 1167 1210
FT DISULFID 1196 1223
FT CARBOHYD 121 121
FT CARBOHYD 339 339
FT CARBOHYD 742 742
FT CARBOHYD 978 978
FT CARBOHYD 1175 1175
SQ SEQUENCE 1268 AA; 137200 MW; 3014E8202A2FAEC CRC64;

Query Match 16.1%; Score 177; DB 1; Length 1268;
Best Local Similarity 31.5%; Pred. No. 7.5e-08;
Matches 45; Conservative 17; Mismatches 49; Indels 32; Gaps 6;

Qy 14 QPCVKVYPHDTGRRLNFEAKACRDGGLVLSIESDEBQKLIKFIENLLPSDGF 73
Db 1048 QGHVY--YF--AHRAWEDAEDCRRAHGLTSVHSPESHKFINSF-----CHENSW 1096
Qy 74 IGLRRREKQSNSTACQDLYAWTDGSGISQFRNXYVDEFS---CGSEVCVVMYHQPSPAG 130
Db 1097 IGLNDRTVRD-----FQWTDNTGLQYENREKQPDNFFAGGEDCVVMVAHESG--- 1145
Qy 131 IGGPMYFQWDRNCRNKNFNICK 153
Db 1146 -----RWNDVPCNLYPVCK 1161

RESULT 5
PCGN HUMAN
ID PCGN HUMAN STANDARD; PRT; 1321 AA.
AC O14594; Q9UPK6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
CN CSRG3 OE NCAN OR NEUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99013874; PubMed=9795216;
RA Prange C.K., Pennacchio L.A., Lieuallen K., Fan W., Lennon G.G.;
RT "Characterization of the human neurocan gene, CSPG3.";
RL Gene 221:199-205(1998).
[2]
RN SEQUENCE OF 1-990 AND 1007-1321 FROM N.A., AND VARIANT ALA-1254.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J., Avila J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomey M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of an ~1 Mb region containing the MEF2B gene in
RP12.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
CC development by binding to neural cell adhesion molecules (NG-CAM
CC and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
CC acid.
CC -!- TISSUE SPECIFICITY: Brain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
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CC -----
CC EMBL; AF026547; AAC80576.1; -
CC EMBL; AC003110; AAB86655.1; -
CC EMBL; AC005254; AAC2581.1; -
CC HSP; P00740; LEDM.
CC Genew; HGNC:2465; CSPG3.
CC MIM; 600826; -
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR00742; EGF_2.
CC InterPro; IPR001881; EGF_CA.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR00538; Link.
CC Pfam; PF00008; Sushi_2.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 2.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 2.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00445; LINK; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 3.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS50026; EGF_3; 2.

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DR PROSITE; PS01187; EGF CA: 1.
DR PROSITE; PS08335; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
KW EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal; Polymorphism.
FT SIGNAL 1 22
FT CHAIN 23 1321
FT DOMAIN 38 153
FT DOMAIN 159 254
FT DOMAIN 260 356
FT DOMAIN 1008 1044
FT DOMAIN 1046 1082
FT DOMAIN 1084 1213
FT DOMAIN 1214 1272
FT DISULFID 59 140
FT DISULFID 182 253
FT DISULFID 206 227
FT DISULFID 280 355
FT DISULFID 304 325
FT DISULFID 1012 1023
FT DISULFID 1017 1032
FT DISULFID 1034 1043
FT DISULFID 1088 1099
FT DISULFID 1116 1208
FT DISULFID 1194 1200
FT DISULFID 1215 1258
FT DISULFID 1244 1271
FT CARBOHYD 122 122
FT CARBOHYD 340 340
FT CARBOHYD 1026 1026
FT CARBOHYD 1223 1223
FT VARIANT 1254 1254
FT CONFLICT 1234 1234
FT CONFLICT 1282 1282
FT SEQUENCE 1321 AA; 142972 MW; 2EF47F823DB980B8 CRC64;

Query Match 16.0%; Score 176; DB 1; Length 1321;
Best Local Similarity 31.5%; Pred. No. 9.6e-08;
Matches 45; Conservative 18; Mismatches 48; Indels 32; Gaps 6;

QY 14 QPCVKVYIYHDTSLRLNFERAKACRRDGGOLYSIEDSEOKLIERFIENLLPSDGF 73
Db 1096 QHCVR--YF--AURRAWDAEKDCRRSHLTVSPHSFNSF-----GHNTW 1144

QY 74 IGLRRREKQNSTACQDLYAWTQGISQFRNWDPEPS---CGSEVCVNYHQPSPAG 130
Db 1145 IGLNDRIVERD-----FQWTDNTGLQFENWENQPDNFFAGGEDCVVVAHESG--- 1193

QY 131 IGGPYMFWNDRCNWKNFICK 153
Db 1194 -----RWNDVPCNLYPYCK 1209

RESULT 6
PCGV BOVIN
ID PCGV BOVIN STANDARD; PRT: 3381 AA.
AC P81282; O77609; O77610; O77611; O77612;
DT 15-DEC-1998 (Rel. 37; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 10-OCT-2003 (Rel. 42; Last annotation update)
DE Versican core protein precursor (large fibroblast proteoglycan)
DE Chondroitin sulfate proteoglycan core protein 2 (PG-M) (Glial
DE hyaluronate-binding protein) (GHAP).
GN CPSC2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS V0; V1; V2 AND V3).
RT TISSUE=Forebrain;

```

```

RX MEDLINE=98288320; PubMed=9624174;
RA Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
RA Zimmermann D.R.;
RT "Versican V2 is a major extracellular matrix component of the mature
RL bovine brain.";
RL J. Biol. Chem. 273:15758-15764 (1998).
RN [2]
RP SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
RP AND 342-348.
RC TISSUE=Spinal cord;
RX MEDLINE=92062692; PubMed=1720020;
RA Perides G., Biviano F., Bignami A.;
RT "Interaction of a brain extracellular matrix protein with hyaluronic
RL acid.";
RL Biochim. Biophys. Acta 1075:248-258 (1991).
CC -I- FUNCTION: May play a role in intracellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -I- SUBUNIT: Interacts with FBLN1 (By similarity).
CC -I- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -I- ALTERNATIVE PRODUCTS:
CC Event-alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=P81282-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=P81282-2; Sequence=VSP_003078, VSP_003079;
CC Name=V2;
CC IsoId=P81282-3; Sequence=VSP_003080;
CC Name=V3;
CC IsoId=P81282-4; Sequence=VSP_003078, VSP_003081;
CC -I- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed
CC in the central nervous system, and in a number of mesenchymal and
CC epithelial tissues; the major isoform V2 is restricted to the
CC central nervous system.
CC -I- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC (By similarity).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -I- SIMILARITY: Contains 2 link domains.
CC -I- SIMILARITY: Contains 2 EGF-like domains.
CC -I- SIMILARITY: Contains 1 C-type lectin family domain.
CC -I- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -I- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC
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CC EMBL; AF060457; AAC24359.1; -
CC EMBL; AF060458; AAC24360.1; -
CC EMBL; AF060459; AAC24361.1; -
CC FIC; T14274; T14274.
CC FIC; T42389; T42389.
CC HSSP; P01132; LEPC.
CC InterPro; IPR000152; Asx_hydroxyl_s.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR007110; IG_Like.
CC InterPro; IPR003599; IG.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00047; IG; 1.
CC Pfam; PF00059; Lectin_c; 1.
CC Pfam; PF00084; sushi; 1.

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PFam; PF00193; Xlink; 2.
DR PRINTS; PRO1265; LINKMODULE.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECK; 1.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00403; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
DR PROSITE; PS00022; EGF 1; 2.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00026; EGF 3; 2.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 3381
FT DOMAIN 21 147
FT DOMAIN 168 245
FT DOMAIN 266 347
FT DOMAIN 349 1336
FT DOMAIN 1337 3074
FT DOMAIN 3074 3110
FT DOMAIN 3112 3148
FT DOMAIN 3161 3275
FT DOMAIN 3280 3338
FT DISULFID 44 131
FT DISULFID 173 244
FT DISULFID 137 218
FT DISULFID 271 346
FT DISULFID 295 316
FT DISULFID 3078 3089
FT DISULFID 3083 3098
FT DISULFID 3100 3109
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FT DISULFID 3154 3165
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FT DISULFID 3310 3327
FT CARBOHYD 57 57
FT CARBOHYD 331 331
FT CARBOHYD 352 352
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FT CARBOHYD 965 965
FT CARBOHYD 1017 1017
FT CARBOHYD 1333 1333
FT CARBOHYD 1337 1393
FT CARBOHYD 1437 1437
FT CARBOHYD 1463 1463
FT CARBOHYD 1653 1653
FT CARBOHYD 1974 1974
FT CARBOHYD 2045 2045
FT CARBOHYD 2074 2074
FT CARBOHYD 2103 2103
FT CARBOHYD 2263 2263
FT CARBOHYD 2290 2290
FT CARBOHYD 2356 2356
FT CARBOHYD 2623 2623
FT CARBOHYD 2641 2641
FT CARBOHYD 2919 2919
FT CARBOHYD 3052 3052
FT CARBOHYD 3354 3354
FT CARBOHYD 3364 3364
FT VARSPLIC 349 349
P -> R (in isoform V1 and isoform V3).

FT VARSPLIC 350 1336
FT VARSPLIC 1337 3074
FT VARSPLIC 350 3074
FT VARSPLIC 350 3074
FT CONFLICT 25 25
FT CONFLICT 51 51
FT CONFLICT 89 89
FT CONFLICT 96 96
FT CONFLICT 346 346
SQ SEQUENCE 3381 AA; 369984 MW; F09716FA7778D459 CRC64;
Query Match 15.9%; Score 174.5; DB 1; Length 3381;
Best Local Similarity 25.5%; Pred. No. 4.2e-07;
Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;
QY 14 QPCKVYIYHDTSRRLNFEBAKACRRDGGQLVSISEDEQKLIKFIENLLPSDGF- 72
DB 3162 QQCCK--YF---AHRRTWDAARECLQGAHLTSLSHEEQHFVRV-----GHYQ 3209
QY 73 WIGLRREEKQNSTACQDLYAWTDGSGISQFRNMYVDEP-----SCSEVCVMYHPSAP 128
DB 3210 WIGL-----NDKMFEDHPRWTDGSTLQVWRPNQDPSFFSTGDCVVIWHENG-- 3259
QY 129 AGIGGPFYFONDDRCNKNFICKYS-----DEKPAVPSREAGE----- 169
DB 3260 -----QWNVPCNHLTYTCKGTVACGPPVVENAKTKGKPRVEINSLRYHC 3310
QY 170 -----ETELTT-----PVL-----PEETOEDAKTKFKESREALN 200
DB 3311 KDGFIQRHLPIRCLGNGRWAMPKXITCLNPSAVQRTYSKKYKNSSSAKDN 3361
RESULT 7
PGCN RAT
ID PGCN RAT STANDARD; PRT; 1257 AA.
AC P5067;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
DE (245 kDa early postnatal core glycoprotein) [Contains: 150 kDa adult
core glycoprotein].
GN CSPG3 OR NCAN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-Sprague-Dawley; TISSUE=Brain;
RM MEDLINE=92406907; PubMed=1326557;
RX Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
RT "Cloning and primary structure of neurocan, a developmentally
regulated, aggregating chondroitin sulfate proteoglycan of brain.";
RL J. Biol. Chem. 267:19536-19547(1992).
RN [2]
RP CHARACTERIZATION.
RM MEDLINE=94230574; PubMed=7513709;
RA Friedlander D.R., Milev P., Karthikeyan L., Margolis R.K.,
RA Margolis R.U., Grumet M.;
RT "The neuronal chondroitin sulfate proteoglycan neurocan binds to the
neural cell adhesion molecules Ng-CAM/11/NELE and N-CAM, and inhibits
neural adhesion and neurite outgrowth.";
RL J. Cell Biol. 125:669-680(1994).
CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
development by binding to neural cell adhesion molecules (NG-CAM
and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
acid.
CC -!- TISSUE SPECIFICITY: Early postnatal and adult brain; not expressed
in kidney, lung, liver and muscle.
CC

[illegible]

RESULT 9
 ID PGCV MOUSE STANDARD; PRT: 3358 AA.
 AC Q62059; Q62058; Q9CUU0;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Versican core protein precursor (large fibroblast proteoglycan)
 DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
 GN CSPG2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS V0; V1 AND V2).
 RC STRAIN=C57BL/6;
 RX MEDLINE=95123551; PubMed=7822336;
 RA Ito K., Shinomura T., Zako M., Ujita M., Kimata K.;
 RT "Multiple forms of mouse PG-M, a large chondroitin sulfate
 proteoglycan generated by alternative splicing.";
 RL J. Biol. Chem. 270:958-965 (1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM V3).
 RC STRAIN=C57BL/6;
 RX MEDLINE=95181355; PubMed=7876137;
 RA Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
 RT "Expression of PG-M(V3), an alternatively spliced form of PG-M
 without a chondroitin sulfate attachment in region in mouse and human
 tissues.";
 RL J. Biol. Chem. 270:3914-3918 (1995).
 RN [3]
 RP SEQUENCE OF 1-1692 FROM N.A. (ISOFORM V1).
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldecelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wallestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.C., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP INTERACTION WITH FBLN1.
 RX MEDLINE=99329059; PubMed=10400671;
 RA Asberg A., Adam S., Kostka G., Timpl R., Heinemann D.;
 RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
 versican.";
 RL J. Biol. Chem. 274:20444-20449 (1999).
 CC -!- FUNCTION: May play a role in intercellular signaling and in
 connecting cells with the extracellular matrix. May take part in

the regulation of cell motility, growth and differentiation. Binds
 hyaluronic acid.
 CC -!- SUBUNIT: Interacts with FBLN1.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=V0;
 CC IsoId=Q62059-1; Sequence=Displayed;
 CC Name=V1;
 CC IsoId=Q62059-2; Sequence=VSP_003087, VSP_003088;
 CC Name=V2;
 CC IsoId=Q62059-3; Sequence=VSP_003089;
 CC Name=V3;
 CC IsoId=Q62059-4; Sequence=VSP_003087, VSP_003090;
 CC -!- TISSUE SPECIFICITY: V2 is found only in brain.
 CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 link domains.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
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 CC
 CC EMBL; D16283; BAA03796.1; -;
 CC EMBL; D28599; -; NOT ANNOTATED CDS.
 CC EMBL; D32040; BAA06802.1; -;
 CC EMBL; AK014525; BAB29411.2; -;
 CC HSSP; P01132; 1EPG.
 CC MGD; MGI:102889; Cspg2.
 CC InterPro; IPR000152; Asx hydroxyl_s.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_CA.
 CC InterPro; IPR006209; EGF-like.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003599; IG.
 CC InterPro; IPR001304; Lectin_C.
 CC InterPro; IPR000338; Link_CCP.
 CC InterPro; IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00047; IG; 1.
 CC Pfam; PF00059; Lectin_c; 1.
 CC Pfam; PF00084; sushi; 1.
 CC Pfam; PF00193; Xlink; 2.
 CC PRINTS; PR01265; LINKMODULE.
 CC ProDom; PD000918; Link; 2.
 CC SMART; SM00032; CCP; 1.
 CC SMART; SM00034; CLECT; 1.
 CC SMART; SM00179; EGF_CA; 1.
 CC SMART; SM00409; IG; 1.
 CC SMART; SM00445; LINK; 2.
 CC PROSITE; PS00010; ASX HYDROXYL; 1.
 CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 CC PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 CC PROSITE; PS00022; EGF_1; 2.
 CC PROSITE; PS01186; EGF_2; 1.
 CC PROSITE; PS00026; EGF_3; 2.
 CC PROSITE; PS01187; EGF_CA; 1.
 CC PROSITE; PS50835; IG LINK; 1.
 CC PROSITE; PS01241; LINK; 2.
 CC Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
 KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
 KW Hyaluronic acid; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 3358
 FT VERSICAN CORE PROTEIN.

RC TISSUE=Brain;
 RX MEDLINE=89174663; PubMed=2466833;
 RA Perides G., Lane W.S., Andrews D., Dahl D., Bignami A.;
 RT "Isolation and partial characterization of a glial
 RT hyaluronate-binding protein.";
 RL J. Biol. Chem. 264:5981-5987(1989).
 RN [9]
 RP TISSUE SPECIFICITY OF ISOFORMS.
 RX MEDLINE=96213482; PubMed=8627343;
 RA Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;
 RT "Differential expression of versican isoforms in brain tumors.";
 RL J. Neuropathol. Exp. Neurol. 55:528-533(1996).
 CC -!- FUNCTION: May play a role in intercellular signaling and in
 CC connecting cells with the extracellular matrix. May take part in
 CC the regulation of cell motility, growth and differentiation. Binds
 CC hyaluronic acid.
 CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing. Named isoforms-5;
 CC Comment=Additional isoforms seem to exist;
 CC Name=V0;
 CC IsoId=PI3611-1; Sequence=Displayed;
 CC Name=V1;
 CC IsoId=PI3611-2; Sequence=VSP_003082, VSP_003083;
 CC Name=V2;
 CC IsoId=PI3611-3; Sequence=VSP_003084;
 CC Name=V3;
 CC IsoId=PI3611-4; Sequence=VSP_003082, VSP_003085;
 CC Name=Vint;
 CC IsoId=PI3611-5; Sequence=VSP_003086;
 CC -!- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed
 CC in normal brain, gliomas, medulloblastomas, schwannomas,
 CC neurofibromas, and meningiomas; V2 is restricted to normal brain
 CC and gliomas; V3 is found in all these tissues except
 CC medulloblastomas.
 CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 link domains.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the agrcan/versican proteoglycan family.
 CC -----
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 CC or send an email to license@sb-sib.ch).
 CC -----
 CC EMBL: U16306; AAA65018.1; -;
 CC EMBL: X15998; CAA34128.1; -;
 CC EMBL: S52488; AAB24878.1; -;
 CC EMBL: U26555; AAA67565.1; -;
 CC EMBL: D32039; BAA06801.1; -;
 CC EMBL: J02814; AAA36437.1; -;
 CC EMBL: AF084545; AAD48545.1; -;
 CC PIR: S06014; A60979.
 CC HSSP: P01132; 1SGF.
 CC Genew: HGNC:2464; CSPG2.
 CC MIM: 118661; -;
 CC GO: GO:0005578; C:extracellular matrix; TAS.
 CC GO: GO:0005540; F:hyaluronic acid binding; TAS.
 CC GO: GO:0008037; P:cell recognition; TAS.
 CC GO: GO:0007275; P:development; TAS.
 CC InterPro: IPR000152; Asx hydroxyl_s.
 CC InterPro: IPR000742; EGF_2.
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR006209; EGF_Like.
 CC InterPro: IPR007110; Ig-Like.
 CC InterPro: IPR003599; Ig.

DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR000538; Link.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00059; Lectin_C; 1.
 DR Pfam: PF00084; sushi; 1.
 DR Pfam: PF00193; Link; 2.
 DR PRINTS: PRO1265; LINKMODULE.
 DR ProDom: PD000918; Link; 2.
 DR SMART: SM00032; CCP; 1.
 DR SMART: SM00034; CLECT; 1.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00409; IG_1.
 DR SMART: SM00445; Link; 2.
 DR PROSITE: PS00010; ASX HYDROXYL; 1.
 DR PROSITE: PS00615; C-TYPE LECTIN 1; 1.
 DR PROSITE: PS00041; C-TYPE LECTIN 2; 1.
 DR PROSITE: PS00022; EGF_1-2.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00026; EGF_3; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00835; IG_Like; 1.
 DR PROSITE: PS01241; Link; 2.
 KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
 KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
 KW Hyaluronic acid; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 3396
 FT DOMAIN 21 146
 FT DOMAIN 167 244
 FT DOMAIN 265 346
 FT DOMAIN 348 1335
 FT DOMAIN 1336 3089
 FT DOMAIN 3089 3125
 FT DOMAIN 3127 3163
 FT DOMAIN 3176 3290
 FT DOMAIN 3295 3353
 FT DISULFID 44 120
 FT DISULFID 172 243
 FT DISULFID 196 217
 FT DISULFID 270 345
 FT DISULFID 294 315
 FT DISULFID 3093 3104
 FT DISULFID 3098 3113
 FT DISULFID 3115 3124
 FT DISULFID 3131 3142
 FT DISULFID 3136 3151
 FT DISULFID 3153 3162
 FT DISULFID 3169 3180
 FT DISULFID 3197 3289
 FT DISULFID 3265 3281
 FT DISULFID 3296 3329
 FT DISULFID 3325 3352
 FT CARBOHYD 57 57
 FT CARBOHYD 330 330
 FT CARBOHYD 615 615
 Query Match 15.8%; Score 174; DB 1; Length 3396;
 Best Local Similarity 28.5%; Pred. No. 4.7e-07;
 Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
 QY 14 QRPCYKVIYFHTGRRRLNFEAKACRRDGGQLVSIIESEDEKLIKFIENLPSDGF- 72
 Db 3177 QCCYK--YF--AHRRTWDAARECRLOGAHLTSILSHEQMFNRV-----GHDYQ 3224
 QY 73 WIGLRREREKQSNSTACQDLVANTDGSISQFRNMYVDEP-----SCGEVCVWYHQPSAP 128
 Db 3225 WIGL-----NDKMFHDPRWTDGTLQYENRPNQPSFFSAGDECVVTHENG-- 3274
 QY 129 AGIGGYPYMFQWNRDRCKMKNFICKYS-----DEXPAVPSREAGE 169
 Db 3275 -----QWNVPCNVHLTYTCKGTGACGQPPVVENAKTFCK 3310

```

RESULT 11
PGCV_CHICK
ID_PGCV_CHICK STANDARD; PRT; 3562 AA.
AC Q90953; Q90945;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
GN CPG2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SOURCE FROM N.A. (ISOFORMS V0 AND V1).
RC STRAIN=White Leghorn; TISSUE=Limb bud;
RX MEDLINE=93300846; PubMed=8314802;
RA Shinomura I., Nishida Y., Ito K., Kinata K.;
RT "CDNA cloning of PG-M, a large chondroitin sulfate proteoglycan
RT expressed during chondrogenesis in chick limb buds. Alternative
RT spliced multiforms of PG-M and their relationships to versican.";
RL J. Biol. Chem. 268:14461-14469(1993).
CC -/- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -/- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -/- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=Q90953-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=Q90953-2; Sequence=VSP_003093;
CC -/- TISSUE SPECIFICITY: Prechondrogenic condensation area of
CC developing limb buds.
CC -/- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC (By similarity).
CC -/- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -/- SIMILARITY: Contains 2 link domains.
CC -/- SIMILARITY: Contains 2 EGF-like domains.
CC -/- SIMILARITY: Contains 1 C-type lectin family domain.
CC -/- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR PFAM; PF00193; Xlink; 2.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; COP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01866; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 26
FT CHAIN 27 3562
FT DOMAIN 27 143
FT DOMAIN 166 243
FT DOMAIN 264 345
FT DOMAIN 3254 3290
FT DOMAIN 3292 3328
FT DOMAIN 3341 3455
FT DOMAIN 3460 3518
FT DISULFID 44 129
FT DISULFID 171 242
FT DISULFID 195 216
FT DISULFID 269 344
FT DISULFID 293 314
FT DISULFID 3258 3269
FT DISULFID 3283 3278
FT DISULFID 3280 3289
FT DISULFID 3296 3307
FT DISULFID 3301 3316
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FT CARBOHYD 235 235
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FT CARBOHYD 1625 1625
FT CARBOHYD 1751 1751
FT CARBOHYD 1988 1988
FT CARBOHYD 2089 2089
FT CARBOHYD 2507 2507
FT CARBOHYD 2642 2642
FT CARBOHYD 2679 2679
FT CARBOHYD 2748 2748
FT CARBOHYD 2762 2762
FT CARBOHYD 3069 3069
FT CARBOHYD 3194 3194
FT CARBOHYD 3232 3232
FT CARBOHYD 3545 3545
FT VARSPPLIC 485 1411
SQ SEQUENCE 3562 AA; 388078 MW; 9BC566B89C1602D2 CRC64;
/FTid=VSP_003093.

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RESULT 13
ID PGCA_BOVIN STANDARD; PRT; 2364 AA.
AC P13608; P79117; Q28159;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSPCP).
GN AGC1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hering T.N., Kollar J., Huynh T.D.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE OF 563-1056 FROM N.A.
RA Antonsson P., Heinigaard D., Oldberg A.;
RX MEDLINE=89380219; PubMed=2528543;
RT "The keratan sulfate-enriched region of bovine cartilage proteoglycan
RT consists of a consecutively repeated hexapeptide motif.";
RL J. Biol. Chem. 264:16170-16173(1989).
RN [3]
RP SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
RX MEDLINE=8727630; PubMed=4111460;
RA Oldberg A., Antonsson P., Heinigaard D.;
RT "The partial amino acid sequence of bovine cartilage proteoglycan,
RT deduced from a cDNA clone, contains numerous Ser-Gly sequences
RT arranged in homologous repeats.";
RL Biochem. J. 243:255-259(1987).
RN [4]
RP SEQUENCE OF 2114-2150 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=93352525; PubMed=8949621;
RA Fueleop C., Walcz E., Valyon M., Glant T.T.;
RT "Expression of alternatively spliced epidermal growth factor-like
RT domains in aggrecans of different species. Evidence for a novel
RT module.";
RL J. Biol. Chem. 268:17377-17383(1993).
RN [5]
RP PARTIAL SEQUENCE.
RX MEDLINE=85027710; PubMed=6489519;
RA Perin J.-P., Bonnet F., Jolles J., Jolles P.;
RT "Sequence data concerning the protein core of the cartilage
RT proteoglycan monomers. Characterization of a sequence allowing the
RT synthesis of an oligonucleotide probe.";
RL FEBS Lett. 176:37-42(1984).
RN [6]
RP PARTIAL SEQUENCE.
RX MEDLINE=87005253; PubMed=3530809;
RA Perin J.P., Bonnet F., Jolles J.;
RT "Structural relationship between link proteins and proteoglycan
RT monomers.";
RL FEBS Lett. 206:73-77(1986).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
CC matrix of cartilaginous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an amino-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P13608-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P13608-2; Sequence=VSP_003072;
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino

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terminus of the proteoglycan, while another globular region, G3,
makes up the C-terminus. G1 contains link domains and thus
consists of three disulfide-bonded loop structures designated as
the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
and the chondroitin sulfate (CS) attachment domains lie between G2
and G3.
CC -!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-
CC LINKED (ABOUT 40) OLIGOSACCHARIDES.
CC -!- PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN
CC ADULT AND FETAL BOVINE PROTEOGLYCANS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U76615; AAB38524.1; -;
CC EMBL; L07053; -; NOT_ANNOTATED_CDS.
CC PIR; A34234; A39808.
CC PIR; T42630; T42630.
CC HSP; P08709; 1BF9.
CC InterPro; IPR002353; Antifreeze1.
CC InterPro; IPR00152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR01881; EGF_Ca.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR003324; SGXSG.
CC InterPro; IPR004336; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 1.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF02339; SGXSG; 61.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 4.
CC PRINTS; PR00356; ANTIFREEZE1.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 4.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00445; LINK; 4.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS50026; EGF_3; 1.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; FALSE_NEG.
CC PROSITE; PS01241; LINK; 4.
CC Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
CC Calcium; Alternative splicing; Repeat; Immunoglobulin domain.
CC SIGNAL
CC Chain 1 16
CC FT CHAIN 17 2364 AGGECAN CORE PROTEIN.
CC DOMAIN 25 147 IG-LIKE V-TYPE.
CC FT DOMAIN 170 247 LINK 1.
CC FT DOMAIN 268 349 LINK 2.
CC FT DOMAIN 504 581 LINK 3.
CC FT DOMAIN 502 683 LINK 4.
CC FT DOMAIN 774 907 23 X 6 AA APPROXIMATE TANDEM REPEATS OF

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FT DOMAIN 1433 2112
 FT FT 2113 2149
 FT DOMAIN 2114 2364
 FT FT 2161 2276
 FT DOMAIN 2280 2338
 FT FT 51 133
 FT DISULFID 175 246
 FT DISULFID 199 220
 FT DISULFID 273 348
 FT DISULFID 297 318
 FT DISULFID 509 580
 FT DISULFID 533 554
 FT DISULFID 607 682
 FT DISULFID 631 652
 FT DISULFID 2117 2128
 FT DISULFID 2182 2274
 FT DISULFID 2250 2266
 FT DISULFID 2281 2324
 FT DISULFID 2310 2337
 FT CARBOHYD 126 126
 FT CARBOHYD 239 239
 FT CARBOHYD 333 333
 FT CARBOHYD 387 387
 FT CARBOHYD 611 611
 FT CARBOHYD 667 667
 FT VARSPLIC 2114 2150
 SQ SEQUENCE 2364 AA; 246359 MW; 6FP83763420C3D4C CRC64;

Query Match 14.4%; Score 158.5; DB 1; Length 2364;
 Best Local Similarity 26.8%; Pred. No. 7.4e-06;
 Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;

QY 6 QPVCRRG---TQPCYKVIYFHD*SRRLNFBFAKACRRDGGVQLVSESDQKLEKFI 62
 Db 2151 QKLCBEGWTKQGHCHYR--HPFD---RATWDAESQCKKQSHLSIVTPEEQ----EFV 2201

QY 63 ENLPSDGF-WIGLRREKQSNSTACQDIYATDGSISQFRWYVDEP-----SCSEV 117
 Db 2202 NN---NAQDYQWIGL-----NDKTIEGDFRWSGHSLSQFNWRPNQDNPFPATGEDC 2250

QY 118 CVMVHPSAPAGIGPYMFWNDRCNMKNFTCKYS---DKPAPVPSKREAGEETE 172
 Db 2251 VMIWHEKG-----EWNDVPCNYQLPFTCKKGTACGPPVVEHARIFGQKD 2298

RESULT 14
 PGCA HUMAN
 ID PGCA HUMAN STANDARD; PRT; 2415 AA.
 AC P16112; Q13650;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP) (Chondroitin sulfate proteoglycan core protein 1).
 GN AGC1 OR CSPG1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Chondrocytes;
 RX MEDLINE=91093289; PubMed=1985970;
 RA Dege K.J., Sasaki M., Kimura T., Yamada Y.;
 RT "Complete coding sequence and deduced primary structure of the human
 RT cartilage large aggregating proteoglycan, aggrecan. Human-specific
 RT repeats, and additional alternatively spliced forms."
 RL J. Biol. Chem. 266:894-902(1991).
 RN [2]
 RP SEQUENCE OF 1778-2415 FROM N.A. (ISOFORM 2).
 RC TISSUE=Chondrocytes;

RA Dudhia J., Hardingham T.E.;
 RL Submitted (JAN-1990) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1936-2415 FROM N.A. (ISOFORM 1).
 RX MEDLINE=89380154; PubMed=2789216;
 RA Baldwin C.T., Reginato A.M., Prockop D.J.;
 RT "A new epidermal growth factor-like domain in the human core protein
 RT for the large cartilage-specific proteoglycan. Evidence for
 RT alternative splicing of the domain."
 RL J. Biol. Chem. 264:15747-15750(1989).
 RN [4]
 RP SEQUENCE OF 764-864 FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95128522; PubMed=7827755;
 RA Barry F.P., Neame P.J., Sasse J., Pearson D.;
 RT "Length variation in the keratan sulfate domain of mammalian
 RT aggrecan."
 RL Matrix Biol. 14:323-328(1994).
 CC -!- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR
 CC MATRIX OF CARTILAGINOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN
 CC IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO
 CC HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION.
 CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=PI6112-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=PI6112-2; Sequence=VSP_003074;
 CC Name=3;
 CC IsoId=PI6112-3; Sequence=VSP_003074, VSP_003075;
 CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
 CC terminus of the proteoglycan, while another globular region, G3,
 CC makes up the COOH terminus. G1 contains link domains and thus
 CC consists of three disulfide-bonded loop structures designated as
 CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
 CC and the chondroitin sulfate (CS) attachment domains lie between G2
 CC and G3.
 CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
 CC chains, N-linked and O-linked oligosaccharides.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 4 link domains.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
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 CC -----
 CC EMBL; M55172; AAA62824.1; -;
 CC EMBL; J05082; AAA35726.1; -;
 CC EMBL; X17406; CAA35463.1; -;
 CC EMBL; S74659; AAC60643.2; -;
 CC FIR; A39086; A39086.
 CC HSSP; P98066; A39086.
 CC Genew; HGNC:319; AGC1.
 CC MIM; 155760;
 CC InterPro; IPR006209; EGF-like.
 CC InterPro; IPR006210; IEGF.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003599; Ig.
 CC InterPro; IPR003006; Ig MHC.
 CC InterPro; IPR001304; Lectin_C.
 CC InterPro; IPR000538; Link.

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InterPro; IPR000436; sushi_SCR_CCP.	
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Pfam; PF00047; ig; 1.	
Pfam; PF00059; lectin_c; 1.	
Pfam; PF02339; SGXSG; 71.	
Pfam; PF00084; sushi; 1.	
Pfam; PF00193; Xlink; 4.	
PRINTS; PR01285; LINKMODULE.	
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SMART; SM00445; LINK; 4.	
PROSITE; PS00615; C-TYPE LECTIN_1; 1.	
PROSITE; PS00641; C-TYPE LECTIN_2; 1.	
PROSITE; PS00022; EGF_1; 1.	
PROSITE; PS01186; EGF_2; 1.	
PROSITE; PS00026; EGF_3; 1.	
PROSITE; PS00835; IG_LIKE; 1.	
PROSITE; PS00290; IG_MHC; 1.	
PROSITE; PS01241; Link; 3.	
Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;	
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LINK	247
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LINK	349
LINK	495
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LINK	593
EGF-LIKE.	673
C-TYPE LECTIN.	2164
SUSHI.	2201
GI-A.	2311
GI-B.	2319
GI-B'.	48
G2-B.	141
G2-B'.	141
K5.	152
CS-1.	247
CS-2.	247
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CS-135.</	

[illegible]

RX MEDLINE=92283265; PubMed=1375914;
 RA Becker-Andre M., van Huijsduijn R.H., Losberger C., Whelan J.,
 RA Delamar J.F.;
 RT "Murine endothelial leukocyte-adhesion molecule 1 is a close
 RT structural and functional homologue of the human protein.";
 RL Eur. J. Biochem. 206:401-411(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92340571; PubMed=1378846;
 RA Weller A., Isenmann S., Vestweber D.;
 RT "Cloning of the mouse endothelial selectins. Expression of both E-
 RT and P-selectin is inducible by tumor necrosis factor alpha.";
 RL J. Biol. Chem. 267:15176-15183(1992).
 CC -!- FUNCTION: Expressed on cytokine induced endothelial cells and
 CC mediates their binding to leukocytes. The ligand recognized by
 CC ELAM-1 is sialyl-Lewis X (alpha1-3)fucosylated derivatives of
 CC polylectamine that are found at the nonreducing termini of
 CC glycolipids.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the selectin/LECAM family.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 6 Sushi (SCR) domains.
 CC -----
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 DR EMBL; M80778; AAA37547.1; -
 DR EMBL; M87862; AAA37577.1; ALT_INIT.
 DR PIR; S23174; B42755.
 DR HSSP; P16581; 1K7A.
 DR MGD; MGI:98278; Sele.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001304; Lectin C.
 DR InterPro; IPR002396; Selectin.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00059; lectin_C; 1.
 DR Pfam; PF00084; sushi; 6.
 DR PRINTS; PR00343; SELECTIN.
 DR SMART; SM00032; CCP; 6.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
 KW Selectin; Signal; Sushi; Repeat.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 612
 FT DOMAIN 22 557 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 558 579
 FT DOMAIN 580 612 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 22 139 C-TYPE LECTIN.
 FT DOMAIN 140 175 EGF-LIKE.
 FT DOMAIN 179 239 SUSHI 1.
 FT DOMAIN 242 301 SUSHI 2.
 FT DOMAIN 304 364 SUSHI 3.
 FT DOMAIN 367 427 SUSHI 4.
 FT DOMAIN 430 490 SUSHI 5.
 FT DOMAIN 493 549 SUSHI 6.
 FT DISULFID 40 138 BY SIMILARITY.
 FT DISULFID 111 130 BY SIMILARITY.
 FT DISULFID 143 154 BY SIMILARITY.
 FT DISULFID 148 163 BY SIMILARITY.

FT DISULFID 165 174 BY SIMILARITY.
 FT DISULFID 180 225 BY SIMILARITY.
 FT DISULFID 210 238 BY SIMILARITY.
 FT DISULFID 243 287 BY SIMILARITY.
 FT DISULFID 273 300 BY SIMILARITY.
 FT DISULFID 305 350 BY SIMILARITY.
 FT DISULFID 336 363 BY SIMILARITY.
 FT DISULFID 368 413 BY SIMILARITY.
 FT DISULFID 399 426 BY SIMILARITY.
 FT DISULFID 431 476 BY SIMILARITY.
 FT DISULFID 462 489 BY SIMILARITY.
 FT DISULFID 494 535 BY SIMILARITY.
 FT DISULFID 521 548 BY SIMILARITY.
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 504 504 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 528 528 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 612 AA; 66749 MW; 86F05713F0EC2C3D CRC64;
 Query Match 14.0%; Score 154.5; DB 1; Length 612;
 Best Local Similarity 27.9%; Pred. No. 3.2e-06;
 Matches 38; Conservative 28; Mismatches 45; Indels 25; Gaps 5;
 QY 22 YHDSIRLNFREAKEACRGGQGVSISEDEQKLEKFIENLLPDSGDFWIGRRREE 81
 Db 23 YYNASSELTYDEASAYCQDYTHLVAIQNKEE---INVLNLSKHSPPYYWIGIRK--- 76
 QY 82 KGSNSTACODLYAWTDGSG---ISQFRNMYVDFFS--CGSEVCVVMVHPQSPAGIGGPTM 136
 Db 77 -----VNNVMIWVGTKPLTEEAQNWAPGNKNQKRNEDCDEIYIQTKDGM----- 124
 QY 137 FQWDDRCNNKNFIC 152
 Db 125 --WNDERCNKKKLC 138

RESULT 17

CD93_MOUSE STANDARD; PRT; 644 AA.
 ID CD93_MOUSE
 AC O89103;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Complement component C1q receptor precursor
 DE subcomponent, receptor 1 (C1qR) (C1qR(p)) (C1q/MBL/SPA receptor)
 GN C1QR1 OR CD93 OR C1QRP OR LY68 OR AA4 (Lymphocyte antigen 68).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=20528605; PubMed=11074255;
 RA Kim T.S., Park M., Nepomuceno R.R., Palmirani G., Winokur S.,
 RA Cotman C.A., Bengtsson U., Tenner A.J.;
 RT "Characterization of the murine homolog of C1qR(P): identical cellular
 RT expression pattern, chromosomal location and functional activity of
 RL the human and murine C1qR(P).";
 RL Mol. Immunol. 37:377-389(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukemia;
 RX MEDLINE=99330438; PubMed=10403644;
 RA Petrenko O., Beavis A., Klaine M., Kittappa R., Godin I.,
 RA Lemischka I.R.;
 RT "The molecular characterization of the fetal stem cell marker AA4.";

[3]
 RN SEQUENCE OF 1956-2124 FROM N.A.
 RP MEDLINE=86250698; PubMed=2424893;
 RA Dorge K., Fernandez P., Hassell J.R., Sasaki M., Yamada Y.;
 RA "Partial cDNA sequence encoding a globular domain at the C terminus
 RT of the rat cartilage proteoglycan";
 RL J. Biol. Chem. 261:8108-8111(1986).
 CC !- FUNCTION: This proteoglycan is a major component of extracellular
 CC matrix of cartilaginous tissues. A major function of this protein
 CC is to resist compression in cartilage. It binds avidly to
 CC hyaluronic acid via an amino-terminal globular region. May play a
 CC regulatory role in the matrix assembly of the cartilage.
 CC !- SUBUNIT: Interacts with PBLN1 (By similarity).
 CC !- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC !- DOMAIN: Two globular domains, G1 and G2, comprise the amino
 CC terminus of the proteoglycan, while another globular region, G3,
 CC makes up the COOH terminus. G1 contains link domains and thus
 CC consists of three disulfide-bonded loop structures designated as
 CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
 CC and the chondroitin sulfate (CS) attachment domains lie between G2
 CC and G3.
 CC !- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
 CC chains, N-linked and O-linked oligosaccharides.
 CC !- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC !- SIMILARITY: Contains 4 link domains.
 CC !- SIMILARITY: Contains 1 C-type lectin family domain.
 CC !- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC !- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
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 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; J13518; AAA41836.1; .
 CC EMBL; M33485; AAA21000.1; ALT_SEQ.
 CC PIR; A92623; A28452.
 CC HSSP; P98066; 17SG.
 CC InterPro; IPR002353; AntifreezeZell.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003006; IG_MHC.
 CC InterPro; IPR003596; IG_V.
 CC InterPro; IPR001304; Lectin_C.
 CC InterPro; IPR000538; Link.
 CC InterPro; IPR003324; SGXSG.
 CC InterPro; IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00059; lectin_c; 1.
 CC Pfam; PF02339; SGXSG; 55.
 CC Pfam; PF00084; sushi; 1.
 CC Pfam; PF00193; Xlink; 4.
 CC PRINTS; PR00356; ANTIFREEZEII.
 CC PRINTS; PR01265; LINKMODULE.
 CC ProDom; PD000918; Link; 4.
 CC SMART; SM00032; CCP; 1.
 CC SMART; SM00034; CLECT; 1.
 CC SMART; SM00406; IGV; 1.
 CC SMART; SM00445; LINK; 4.
 CC PROSITE; PS00615; C-TYPE_LLECTIN_1; 1.
 CC PROSITE; PS00641; C-TYPE_LLECTIN_2; 1.
 CC PROSITE; PS00835; IG LIKE; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PROSITE; PS01241; LINK; 4.
 CC Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; Repeat;
 CC Immunoglobulin domain.
 KW SIGNAL 1 19 POTENTIAL.
 KW CHAIN 20 2124 AGGREGAN CORE PROTEIN.
 FT DOMAIN 34 147
 FT LINK 1.
 FT DOMAIN 170 247

FT DOMAIN 268 349 LINK 2.
 FT DOMAIN 504 581 LINK 3.
 FT DOMAIN 602 683 LINK 4.
 FT DOMAIN 1910 2036 C-TYPE LECTIN.
 FT DOMAIN 2040 2098 SUSHI.
 FT DOMAIN 48 140 G1-A.
 FT DOMAIN 152 247 G1-B.
 FT DOMAIN 253 349 G1-B'.
 FT DOMAIN 486 580 G2-B.
 FT DOMAIN 587 682 G2-B'.
 FT DOMAIN 685 798 KS.
 FT DOMAIN 801 1226 CS-1.
 FT DOMAIN 1227 1909 CS-2.
 FT DOMAIN 1910 2124 G3.
 FT DISULFID 51 133 BY SIMILARITY.
 FT DISULFID 175 246 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT DISULFID 273 348 BY SIMILARITY.
 FT DISULFID 297 318 BY SIMILARITY.
 FT DISULFID 509 580 BY SIMILARITY.
 FT DISULFID 533 554 BY SIMILARITY.
 FT DISULFID 607 682 BY SIMILARITY.
 FT DISULFID 631 652 BY SIMILARITY.
 FT DISULFID 1914 1925 BY SIMILARITY.
 FT DISULFID 1942 2034 BY SIMILARITY.
 FT DISULFID 2010 2026 BY SIMILARITY.
 FT DISULFID 2041 2084 BY SIMILARITY.
 FT DISULFID 2070 2097 BY SIMILARITY.
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 667 667 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1842 1842 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 2124 AA; 221117 MW; E30BBE61593A34B1 CRC64;

Query Match 14.0%; Score 153.5; DB 1; Length 2124;
 Best Local Similarity 26.3%; Pred. No. 1.8e-05;
 Matches 47; Conservative 27; Mismatches 62; Indels 43; Gaps 9;

QY 6 QPVCROG---TORPCVKVIYFHDTSRLNFEBAKACRRDGGQLVISEDQKLEKEI 62
 Db 1911 QEQCEGWTKFGHCYR--HFPD---RETWDAERRCRQQSHLSIVTFPEQEFYNKNA 1965
 QY 63 ENLLPSDGF-WIGLRRREKQSNSTACODLVAWTGDSISQFRNWWVDEP---SCGSEV 117
 Db 1966 Q-----DYQWIGL-----NRTIEGDFWSDGSHLQFEKWRPNQDPFATGDC 2010
 QY 118 CVVMYHQPSAPAGIGGYPYFQWDDRCNMKNFICKYS----DEKPAVPSREAEGETE 172
 Db 2011 VVMWHERG-----ENNDVPCNVQLPFTCKGTGTVACGEPPEVHARTLGQKD 2058

RESULT 19
 PGCB_BOVIN
 ID PGCB_BOVIN STANDARD; PRT; 912 AA.
 AC Q28062;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Brevican core protein precursor.
 GN BCAN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RC SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP TISSUE=Brain;
 RX MEDLINE=94193597; PubMed=8144512;
 RA Yamada H., Watanabe K., Shimonaka M., Yamaguchi Y.;

"Molecular cloning of brevican, a novel brain proteoglycan of the aggrecan/versican family." J. Biol. Chem. 269:10119-10126(1994).

CC -!- FUNCTION: May play a role in the terminally differentiating and the adult nervous system during postnatal development. Could stabilize interactions between HA and brain proteoglycans.

CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).

CC -!- TISSUE SPECIFICITY: Brain; expressed in cerebellar astrocytes but not in neurons.

CC -!- PTM: Contains mostly chondroitin sulfate.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- SIMILARITY: Contains 2 link domains.

CC -!- SIMILARITY: Contains 1 EGF-like domain.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.

CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

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DR EMBL; X75887; CA53481.1; -

DR PIR; A54423; A54423.

DR HSP; P20693; 1HLJ.

DR InterPro; IPR002353; AntifreezeII.

DR InterPro; IPR00742; EGF 2.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig V.

DR InterPro; IPR001304; Lectin_C.

DR InterPro; IPR000538; Link.

DR InterPro; IPR000436; Sushi_SCR_CCP.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00047; Ig; 1.

DR Pfam; PF00059; lectin_c; 1.

DR Pfam; PF00084; sushi; 1.

DR Pfam; PF00193; Xlink; 2.

DR PRINTS; PR00356; ANTIFREEZEII.

DR PRINTS; PR01285; LINKMODULE.

DR PRODOM; PD000918; Link; 2.

DR SMART; SM00032; CCP; 1.

DR SMART; SM00034; CLECT; 1.

DR SMART; SM00181; EGF; 1.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00445; LINK; 2.

DR PROSITE; PS00815; C-TYPE LECTIN_1; 1.

DR PROSITE; PS00841; C-TYPE LECTIN_2; 1.

DR PROSITE; PS00022; EGF 1; 1.

DR PROSITE; PS01186; EGF 2; 1.

DR PROSITE; PS00266; EGF 3; 1.

DR PROSITE; PS00835; IG LIKE; 1.

DR PROSITE; PS00290; IG MHC; 1.

DR PROSITE; PS01241; LINK; 2.

KW Glycoprotein; Hyaluronic acid; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain; Repeat; Immunoglobulin domain.

FT SIGNAL 1 22

FT CHAIN 23 912

FT DOMAIN 36 155

FT DOMAIN 174 251

FT DOMAIN 272 353

FT DOMAIN 647 683

FT DOMAIN 693 811

FT DOMAIN 812 876

FT DOMAIN 57 137

FT DISULFID 179 250

FT DISULFID 203 224

FT DISULFID 277 352 BY SIMILARITY.

FT DISULFID 301 322 BY SIMILARITY.

FT DISULFID 651 662 BY SIMILARITY.

FT DISULFID 656 671 BY SIMILARITY.

FT DISULFID 673 682 BY SIMILARITY.

FT DISULFID 689 700 BY SIMILARITY.

FT DISULFID 717 809 BY SIMILARITY.

FT DISULFID 785 801 BY SIMILARITY.

FT DISULFID 816 859 BY SIMILARITY.

FT DISULFID 845 872 BY SIMILARITY.

FT CARBOHYD 130 130 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 337 337 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 912 AA; 99554 MW; 677B3EB1C688C4D7 CRC64;

Query Match 13.8%; Score 152; DB 1; Length 912;

Best Local Similarity 28.8%; Pred. No. 8.7e-06;

Matches 47; Conservative 17; Mismatches 61; Indels 38; Gaps 8;

QY 14 QPCVKVYFHDTSRLNFEAKERDGGOLVSEDEQKLEKFIENLLPSDGF 73

DB 697 QGACYK----HPSARR-SWEAEAKRMVGAHLASISPEEQDFINRYREVQ-----W 745

QY 74 IGLRRREKQSNSTACQDIYAWTDSISQFRWYVDPS---CGSEVCVM-YHPSAPA 129

DB 746 IGL-----NDRTIEGDFLWSDGVPLLYENWNPQDPVSFLSGENCVMVWHQDQ--- 794

QY 130 GIGGPMFQWDDRCNMKNFKYKYS---DEKPAVPSREAE 168

DB 795 -----QWSDVPCNYHLSTCKMGLVSCGPPPLAEVFG 829

RESULT 20

CD93 HUMAN STANDARD; PRT; 652 AA.

AC Q9NPY3; O00274;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Complement component C1q receptor precursor (Complement component 1, q subcomponent, receptor 1) (C1qR) (C1qR(p)) (C1q/MBL/SPA receptor)

DE (CD93 antigen) (CDW93).

GN C1QR1 OR CD93.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RA MEDLINE=97199258; PubMed=9047234;

RA Nepomuceno R.R., Henschen-Edman A.H., Burgess W.H., Tenner A.J.; "CDNA cloning and primary structure analysis of C1qR(p), the human C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro."; Immunity 6:119-129(1997).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANT ALA-318.

RA MEDLINE=21640567; PubMed=11781389;

RA Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N., Prager E., Stafler G., Madic O., Stockinger H., Knapp W.; "Identification of human CD93 as the phagocytic C1q receptor (C1qR) by expression cloning."; J. Leukoc. Biol. 71:133-140(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=21638749; PubMed=11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.F., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

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EMBL; U94333; AAB53110.1; --
EMBL; ALI18508; CAC00597.1; --
EMBL; BC028075; AAH28075.1; --
HSSP; P35555; IEMN.
Genew; HGNC:15855; CLQR1.
MIM; 120577; --
GO; GO:0016021; C:integral to membrane; IC.
GO; GO:0004872; F:receptor activity; NAS.
GO; GO:0016337; P:cell-cell adhesion; IDA.
GO; GO:0042116; P:macrophage activation; NAS.
GO; GO:0006909; P:phagocytosis; NAS.
InterPro; IPRO00152; ASx_hydroxyl_S.
InterPro; IFRO01881; EGF_CA.
InterPro; IFRO06209; EGF-like.
InterPro; IFRO01304; Lectin_C.
Pfam; PF00008; EGF; 5.
PFAM; PF00059; lectin_c; 1.
SMART; SM00034; CLECT_1.
SMART; SM00179; EGF_CA; 3.
PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS00519; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS00026; EGF_3; 3.
PROSITE; PS01187; EGF_CA; 3.
Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
EGF-like domain; Lectin; Glycoprotein; Polymorphism.

SIGNAL	1	21
CHAIN	22	652
DOMAIN	24	580
TRANSFMEN	581	601
DOMAIN	602	652
DOVAIN	32	174
DOVAIN	260	301
DOVAIN	302	344
DOVAIN	345	384
DOVAIN	385	426
DOVAIN	427	468
DOVAIN	594	601
DLSULFD	264	275
DLSULFD	271	285
DLSULFD	287	300
DLSULFD	306	317
DLSULFD	311	328
DLSULFD	330	343
DLSULFD	349	358
DLSULFD	354	367
DLSULFD	369	383
DLSULFD	389	400
DLSULFD	396	409
DLSULFD	411	425
DLSULFD	431	443
DLSULFD	439	452
DLSULFD	454	467
CARBOHYD	325	325
VARIANT	318	318

COMPLEMENT COMPONENT C1Q RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5. CALCIUM-BINDING (POTENTIAL).
POLY-LEU.
BY SIMILABILITY.
BY SIMILABILITY.
BY SIMILABILITY.
BY SIMILABILITY.
BY SIMILABILITY.
BY SIMILABILITY.
BY SIMILABILITY.
BY SIMILABILITY.
BY SIMILABILITY.
BY SIMILABILITY.
BY SIMILABILITY.
N-LINKED (GLCNAC...) (POTENTIAL).
V -> A.
/*Fid=VAR_013573.
T -> V (IN REF. 1; AA SEQUENCE).
C -> T (IN REF. 1; AA SEQUENCE).
TA -> RI (IN REF. 1; AA SEQUENCE).
S -> N (IN REF. 1; AA SEQUENCE).
G -> A (IN REF. 1; AA SEQUENCE).
S -> A (IN REF. 1; AA SEQUENCE).
R -> Q (IN REF. 1; AA SEQUENCE).
R -> G (IN REF. 1; AA SEQUENCE).
CONFLICT 22 22
CONFLICT 36 36
CONFLICT 38 39
CONFLICT 155 155
CONFLICT 186 186
CONFLICT 492 492
CONFLICT 496 496
CONFLICT 504 504

Graham D.V., Griffiths C., Griffiths M.N.D., William R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Hoiden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekesch K., Johnson C.M., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaeslaiho M.H., Lervsha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Tracey A., Iromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
Whitehead S.B., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20";
Nature 414:865-871(2001).
[4].
SEQUENCE FROM N.A.
TISSUE=Leukocyte;
MEDLINE=23388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusica K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5].
CHARACTERIZATION.
MEDLINE=21990337; PubMed=11994479;
McGreal E.P., Ikwaki N., Akatsu H., Morgan B.P., Gasque P.;
"Human C1qR is identical with CD93 and the mni-11 antigen but does
not bind C1q";
J. Immunol. 169:5222-5232(2002).
[6].
O-GLYCOSYLATION.
MEDLINE=9919277; PubMed=10092817;
Nepomuceno R.R., Ruiz S., Park M., Tenner A.J.;
"C1qR is a heavily O-glycosylated cell surface protein involved in
the regulation of phagocytic activity";
J. Immunol. 162:3583-3589(1999).
-!- FUNCTION: Receptor (or element of a larger receptor complex) for
protein A (SPA). May mediate the enhancement of phagocytosis in
monocytes and macrophages upon interaction with soluble defense
collagens. May play a role in intercellular adhesion.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Highly expressed in endothelial cells,
platelets, cells of myeloid origin, such as monocytes and
neutrophils. Not expressed in cells of lymphoid origin.
-!- PTM: N- and O-glycosylated.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 5 EGF-like domains.
-!- CAUTION: Has been sometimes referred to as a collectin receptor.
-!- DATABASE: NAME=PROW; NOTE=PROW 3:1-6(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/467246456.g.htm".

RA Suemura M., Kishimoto T.;
RT "Two species of human Fc epsilon receptor II (Fc epsilon RII/CD23):
RL tissue-specific and IL-4-specific regulation of gene expression."
RN Cell 55:611-618(1988).
RP [6]
RX 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
RY MEDLINE=94191542; PubMed=8142907;
RA Padlan E.A., Helm B.A.;
RT "Modeling of the lectin-homology domains of the human and murine low-
RL affinity Fc epsilon receptor (Fc epsilon RII/CD23).";
RN Receptor 3:325-341(1993).
RP [7]
RX 3D-STRUCTURE MODELING OF 173-285.
RY MEDLINE=96276216; PubMed=8745401;
RA Bajorath J., Aruffo A.;
RT "Structure-based modeling of the ligand binding domain of the human
RL cell surface receptor CD23 and comparison of two independently
RN derived molecular models";
RX Protein Sci. 5:240-247(1996).
RY -!- FUNCTION: This receptor has essential roles in the regulation of
RL IgE production and in the differentiation of B-cells (it is a B-
RN cell-specific antigen).
RY -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS A
RN -!- SOLUBLE EXCRETED FORM.
RY -!- ALTERNATIVE PRODUCTS.
RN Name=A;
RX Event=Alternative splicing; Named isoforms=2;
RY Name=B;
RX IsoId=P06734-1; Sequence=Displayed;
RY IsoId=P06734-2; Sequence=VSP_003057;
RX -!- PTM: N- and O-glycosylated.
RY -!- MISCELLANEOUS: There are two kinds of Fc receptors for IgE, which
RN differ in both structure and function: high affinity receptors on
RX basophils and mast cells and low affinity receptors on lymphocytes
RY and monocytes.
RN -!- SIMILARITY: Contains 1 C-type lectin family domain.
RX -!- DATABASE: NAME=PROW; NOTE=CD guide CD23 entry;
RY WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd23.htm".
RN -----
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RY between the Swiss Institute of Bioinformatics and the EMBL outstation
RN the European Bioinformatics Institute. There are no restrictions on its
RX use by non-profit institutions as long as its content is in no way
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RX or send an email to license@isb-sib.ch).
RY -----
DR EMBL; M15059; AAA52434.1; -;
DR EMBL; M14766; AAA52435.1; -;
DR EMBL; X04772; CAA28465.1; -;
DR EMBL; M23562; AAA52433.1; -;
DR PIR; A26087; LNHUER.
DR PDB; 1HLI; 31-JAN-94.
DR PDB; 1KJE; 03-APR-96.
DR Genew; HGNC:3612; FCER2.
DR MIM; 151445; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005178; F:integrin binding; TAS.
DR InterPro; IPR002353; AntiFreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
KW Receptor; Antigen; IgE-binding protein; Repeat; Signal-anchor;
RN Transmembrane; Lectin; Glycoprotein; Alternative splicing;
KW 3D-structure.
FT CHAIN 1 321 MEMBRANE BOUND FORM.
FT CHAIN 150 321 SOLUBLE FORM.
FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT TRANSMEM 22 47 SIGNAL-ANCHOR (POTENTIAL).

FT DOMAIN 48 321 EXTRACELLULAR (POTENTIAL).
FT SITE 152 284 C-TYPE LECTIN (LONG FORM).
FT REPEAT 69 89 CLEAVAGE.
FT REPEAT 90 110
FT REPEAT 111 131
FT DISULFID 160 288
FT DISULFID 163 174
FT DISULFID 191 282
FT DISULFID 239 273
FT CARBOHYD 63 63
FT VARSGLYIC 1 7
FT CONFLICT 269 269
FT STRAND 174 177
FT HELIX 184 193
FT TURN 194 195
FT STRAND 197 198
FT HELIX 204 214
FT TURN 215 216
FT STRAND 219 228
FT TURN 229 230
FT STRAND 231 234
FT TURN 235 236
FT STRAND 239 239
FT STRAND 245 245
FT TURN 247 248
FT TURN 254 255
FT STRAND 259 282
FT TURN 264 285
FT STRAND 268 271
FT TURN 273 274
FT STRAND 281 284
SQ SEQUENCE 321 AA; 36468 MW; F86708C0E6515B87 CRC64;
Query Match 13.5%; Score 149; DB 1; Length 321;
Best Local Similarity 30.2%; Pred.No. 4.5e-06;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;
QY 14 QRPYKVIYFHDTSRLNFEAKEACRDGGOLVSISEDEQKLEKFIENLLPSDGF 73
DB 171 QRKCY---YFGKTKQ--VWHARYACDDMEGLVSIHSPEQDFTLTKH-----ASHTGSW 220
QY 74 IGLRREEQKSNSTACQDIYANTDGSISQFRNYYVDPESCGS--EYCVVMYHQPAPAGI 131
DB 221 IGLRLDLKGE-----FIWYDGSVDYSNWAPEPTSRSGQEDCVVM-----RGS 265
QY 132 GGPYMFQWDDRCNMK--NNFICKYDEKPAV---PSREAEGE-----ETELTPV 177
DB 266 G-----RWDAFCDRKLGAVC-----DRLATCTPPASEGSAEGMGPDSRDPDGLRPTPS 316
QY 178 LP 179
DB 317 AP 316
RESULT 23
PGCA MOUSE
ID PGCA MOUSE STANDARD; PET; 2132 AA.
AC Q61282; Q64021;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSGPCP).
GN AGC1 OR AGC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c; TISSUE=Cartilage;

RX MEDLINE=95104847; PubMed=7806222;
 RA Walcz E., Deak F., Ehardt F., Coulter S.N., Fuellep C., Horvath P.,
 Doege K.J., Giant T.T.;
 RT "Complete coding sequence, deduced primary structure, chromosomal
 localization, and structural analysis of murine aggrecan.";
 RL Genomics 22:364-371(1994).
 RN [2]
 RP SEQUENCE OF 211-326 FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=95004579; PubMed=7920633;
 RA Watanabe H., Kimata K., Line S., Strong D., Gao L.-Y., Kozak C.A.,
 Yamada Y.;
 RT "Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in
 the aggrecan gene.";
 RL Nat. Genet. 7:154-157(1994).
 RN [3]
 RP INTERACTION WITH FBLN1.
 RX MEDLINE=99329059; PubMed=10400671;
 RA Asberg A., Adam S., Kostka G., Timml R., Heinigaard D.;
 RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
 versican.";
 RL J. Biol. Chem. 274:20444-20449(1999).
 CC -!- FUNCTION: This proteoglycan is a major component of extracellular
 matrix of cartilaginous tissues. A major function of this protein
 is to resist compression in cartilage. It binds avidly to
 hyaluronic acid via an amino-terminal globular region. May play a
 regulatory role in the matrix assembly of the cartilage.
 CC -!- SUBUNIT: Interacts with FBLN1.
 CC -!- SUPRACELLULAR LOCATION: Secreted; extracellular matrix (By
 similarity).
 CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
 terminus of the proteoglycan, while another globular region, G3,
 makes up the COOH terminus. G1 contains link domains and thus
 consists of three disulfide-bonded loop structures designated as
 the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
 and the chondroitin sulfate (CS) attachment domains lie between G2
 and G3.
 CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
 chains, N-linked and O-linked oligosaccharides.
 CC -!- DISEASE: Defects in AGC1 are the cause of cartilage matrix
 deficiency (CMD). CMD is an autosomal recessive syndrome
 characterized by cleft palate, short limbs, tail and snout.
 CC Mutation in strain CMD causes absence of aggrecan by truncation of
 the protein (mutation in the G1 domain).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 4 link domains.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L07049; AAC37670.1; --
 CC EMBL; S73722; AAB32160.1; --
 CC EMBL; S73721; AAB32160.1; JOINED.
 CC PIR; A55182; A55182.
 CC HSPSP; P98066; 1TSG.
 CC MGD; MGI:99602; Agcl.
 CC InterPro; IPR002353; Antifreeze1.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003006; Ig MHC.
 CC InterPro; IPR003596; Ig v.
 CC InterPro; IPR001304; Lectin_C.
 CC InterPro; IPR005538; Link.
 CC InterPro; IPR003324; SGXSG.
 CC InterPro; IPR000436; Sushi_SCR_OCP.

DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF02339; SGXSG; 60.
 DR Pfam; PF00084; sushi; 1.
 DR Pfam; PF00193; xlink; 4.
 DR PRINTS; PRO0356; ANTIFREEZE1.
 DR PRINTS; PRO1265; LINKMODULE.
 DR ProDom; PD000918; Link; 4.
 DR SMART; SM00032; CCP; 1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SMC00406; IGV; 1.
 DR SMART; SMC0445; LINK; 4.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE; PS00441; C-TYPE LECTIN_2; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00290; IG MHC; 1.
 DR PROSITE; PS01241; LINK; 4.
 DR Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; Repeat;
 KW Immunoglobulin domain.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 2132 AGGREGAN CORE PROTEIN.
 FT DOMAIN 34 147 IG-LIKE V-TYPE.
 FT DOMAIN 170 247 LINK 1.
 FT DOMAIN 268 349 LINK 2.
 FT DOMAIN 504 581 LINK 3.
 FT DOMAIN 602 683 LINK 4.
 FT DOMAIN 1918 2044 C-TYPE LECTIN.
 FT DOMAIN 2048 2106 SUSHI.
 FT DOMAIN 48 140 GI-A.
 FT DOMAIN 152 247 GI-B.
 FT DOMAIN 253 349 GI-B'.
 FT DOMAIN 486 580 G2-B.
 FT DOMAIN 587 682 G2-B'.
 FT DOMAIN 685 803 KS.
 FT DOMAIN 805 1231 CS-1.
 FT DOMAIN 1232 1917 CS-2.
 FT DOMAIN 1917 2132 G3.
 FT DISULFID 51 133 BY SIMILARITY.
 FT DISULFID 175 246 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT DISULFID 273 348 BY SIMILARITY.
 FT DISULFID 297 318 BY SIMILARITY.
 FT DISULFID 509 580 BY SIMILARITY.
 FT DISULFID 533 554 BY SIMILARITY.
 FT DISULFID 607 682 BY SIMILARITY.
 FT DISULFID 631 652 BY SIMILARITY.
 FT DISULFID 1922 1933 BY SIMILARITY.
 FT DISULFID 1950 2042 BY SIMILARITY.
 FT DISULFID 2018 2034 BY SIMILARITY.
 FT DISULFID 2049 2092 BY SIMILARITY.
 FT DISULFID 2078 2105 BY SIMILARITY.
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 667 667 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1675 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 1171 1173 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 2132 AA; 222008 MW; 0B2BCDFC6CDBA163 CRC64;
 Query Match 13.4%; Score 147.5; DB 1; Length 2132;
 Best Local Similarity 24.7%; Pred. No. 6.3e-05;
 Matches 45; Conservative 30; Mismatches 64; Indels 43; Gaps 9;
 QY 3 LSGQPVCRGG---TQPCYKVIYFHTSRRLNPFEEAKCRDGGQGVSESEDEKLE 59
 Db 1916 VADQCEEGWTKFGHCYR-HPFD---RETWDAERRCREQSHLSIVTPEQSFVN 1970
 QY 60 KFENLPSDGF-WIGLRREKQSNSTACQDIYANTDGSISQFRWYVDEP-----SCG 114
 Db 1971 KNAQ-----DYQWIGL-----NDRITTEGFRWSDGHSLOFEKWRPNQPNFFATG 2015

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Qy 115 SEVGVVYHPSAPAGIGGPMFQWDDRCNMKNFICKYS-----DEKPAVPSRAEGEE 170
Db 2016 EDCVMIWHERG-----EWNDVPCNYQLPFTCKGTACGDPFVVEHARTLGQK 2064
Qy 171 TE 172
Db 2065 KD 2066

RESULT 24
PCGB MOUSE STANDARD; PRT; 883 AA.
AC 061361;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Brevican core protein precursor.
GN BCAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=97432816; PubMed=9286696;
RA Rauch U., Meyer H., Brakebusch C., Seidenbecher C., Gundelfinger E.D.,
RA Beier D.R., Fassler R.;
RT "Sequence and chromosomal localization of the mouse brevican gene.";
CC CC -!- FUNCTION: May play a role in the terminally differentiating and
the adult nervous system during postnatal development. Could
stabilize interactions between HA and brain proteoglycans.
CC CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
similarity).
CC CC -!- TISSUE SPECIFICITY: Brain (By similarity).
CC CC -!- PTM: Contains mostly chondroitin sulfate (By similarity).
CC CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC CC -!- SIMILARITY: Contains 2 link domains.
CC CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

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EMBL; X87096; CAA60575.1; -.
DR PIR, S57653; S57653.
DR HSP; P20693; 1HLJ.
DR MGD; MGI:1096385; Bcan.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; Xlink; 2.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR01265; LINKMODULE.
```

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DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS00441; C-TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Hyaluronic acid; Proteoglycan; Lectin; Signal; Sushi;
KW EGF-like domain; Repeat; Immunoglobulin domain.
FT SIGNAL 1 22
FT CHAIN 23 883
FT DOMAIN 35 154
FT DOMAIN 171 250
FT DOMAIN 271 352
FT DOMAIN 622 658
FT DOMAIN 658 786
FT DOMAIN 787 851
FT DOMAIN 56 136
FT DISULFID 178 249
FT DISULFID 202 223
FT DISULFID 276 351
FT DISULFID 300 321
FT DISULFID 625 637
FT DISULFID 631 646
FT DISULFID 648 657
FT DISULFID 664 675
FT DISULFID 692 784
FT DISULFID 760 776
FT DISULFID 791 834
FT DISULFID 820 847
FT CARBOHYD 129 129
FT CARBOHYD 336 336
SQ SEQUENCE 883 AA; 96013 MW; CC2C3C97B453E45 CRC64;

Query Match 13.4%; Score 147; DB 1; Length 883;
Best Local Similarity 29.7%; Pred. No. 2.4e-05;
Matches 43; Conservative 21; Mismatches 45; Indels 36; Gaps 8;

Qy 14 QRCYKVIYFHTSRLENFEAEKACRRGGQGLVSTESDEQKLI-EKTIENLLPSDGF 72
Db 672 QGACYK---HFSTR-SWEAEASQCALGAHLTSCTPEEQDFVNDRYEQ----- 719
Qy 73 WIGLRREEKQSNSTACQDLVAMTDGSIQFRNRYVDEPS---CGSEVCVM-YHQPSAP 128
Db 720 WIGL-----NDRIEGDFLWSDGAPLLYENWNPQDPDSYFLSGENCVMVWHDQG-- 769
Qy 129 AGIGGPMFQWDDRCNMKNFICK 153
Db 770 -----QWSDVPCNYHLSYCK 785

RESULT 25
PCGA CHICK STANDARD; PRT; 2109 AA.
AC P07898; Q90810; Q90820; Q90991; Q91047;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
protein) (CSPCP).
GN AGCI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
```

RN SEQUENCE FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Embryo;
 RX MEDLINE=94043149; PubMed=8226878;
 RA Li H., Schwartz N.B., Vertel B.M.;
 RT "CDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core
 RT protein and identification of a stop codon in the aggrecan gene
 RT associated with the chondrodysplasia, nanomelia.";
 RL J. Biol. Chem. 268:23504-23511(1993).
 RN [2]
 RP SEQUENCE OF 1042-1559 FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=90307744; PubMed=1694853;
 RA Krueger R.C. Jr., Fields T.A., Mensch J.R. Jr., Schwartz N.B.;
 RT "Chick cartilage chondroitin sulfate proteoglycan core protein. II.
 RT Nucleotide sequence of cDNA clone and localization of the S103L
 RT epitope.";
 RL J. Biol. Chem. 265:12088-12097(1990).
 RN [3]
 RP SEQUENCE OF 1-1855 AND 1893-2109 FROM N.A.
 RC TISSUE=Cartilage;
 RX MEDLINE=93111968; PubMed=1339285;
 RA Chandrasekaran L., Tanzer M.L.;
 RT "Molecular cloning of chicken aggrecan. Structural analyses.";
 RL Biochem. J. 288:903-910(1992).
 RN [4]
 RP ERRATUM.
 RX MEDLINE=94107258; PubMed=8280087;
 RA Chandrasekaran L., Tanzer M.L.;
 RL Biochem. J. 296:885-887(1993).
 RN [5]
 RP SEQUENCE OF 1492-1610 FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Chondrocytes;
 RX MEDLINE=95128519; PubMed=7827752;
 RA Primorac D., Stover M.L., Clark S.H., Rowe D.W.;
 RT "Molecular basis of nanomelia, a heritable chondrodysplasia of
 RT chicken.";
 RL Matrix Biol. 14:297-305(1994).
 RN [6]
 RP SEQUENCE OF 1894-2109 FROM N.A.
 RX MEDLINE=89008500; PubMed=3170613;
 RA Tanaka T., Har-El R., Tanzer M.L.;
 RT "Partial structure of the gene for chicken cartilage proteoglycan
 RT core protein.";
 RL J. Biol. Chem. 263:15831-15835(1988).
 RN [7]
 RP SEQUENCE OF 1693-1855 AND 1893-2109 FROM N.A.
 RX MEDLINE=86259736; PubMed=3460082;
 RA Sai S., Tanaka T., Koshier R.A., Tanzer M.L.;
 RT "Cloning and sequence analysis of a partial cDNA for chicken
 RT cartilage proteoglycan core protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5081-5085(1986).
 CC -!- FUNCTION: This proteoglycan is a major component of extracellular
 CC matrix of cartilaginous tissues. A major function of this protein
 CC is to resist compression in cartilage. It binds avidly to
 CC hyaluronic acid via an amino-terminal globular region. May play a
 CC regulatory role in the matrix assembly of the cartilage.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P07898-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P07898-2; Sequence=VSP_003073;
 CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
 CC terminus of the proteoglycan, while another globular region, G3,
 CC makes up the COOH terminus. G1 contains link domains and thus
 CC consists of three disulfide-bonded loop structures designated as
 CC the A, B, C motifs. G2 is similar to G1. The keratan sulfate (KS)
 CC and the chondroitin sulfate (CS) attachment domains lie between G2
 CC and G3.
 CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate

CC chains, N-linked and O-linked oligosaccharides.
 CC -!- DISEASE: DEFECTS IN AGC1 ARE THE CAUSE OF NANOMELIA, A LETHAL
 CC CONNECTIVE TISSUE DISORDER AFFECTING CARTILAGE DEVELOPMENT
 CC (CHONDRODYSPLASIA) CHARACTERIZED BY SHORTENED AND MALFORMED LIMBS.
 CC AGGREGAN IS TRUNCATED AT ITS C-TERMINAL IN THE CS-2 BINDING DOMAIN
 CC AND IS NOT ANMORE SECRETED FROM THE CHONDROCYTES.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 4 link domains.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -----
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 CC -----
 CC EMBL; L21913; AAB19128.1; -;
 CC EMBL; M38187; AAA48731.1; -;
 CC EMBL; M88101; -; NOT ANNOTATED_CDS.
 CC EMBL; S74657; AAC60751.1; JOINED.
 CC EMBL; S74656; AAC60751.1; JOINED.
 CC EMBL; J04028; AAA48719.1; -;
 CC EMBL; M13993; AAA48720.1; -;
 CC PIR; I50421; I50421.
 CC HSP; P08709; IBF9.
 CC InterPro; IPR002353; AntifreezeZell.
 CC InterPro; IPR000152; Asx_hydroxyl_s.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003599; IG.
 CC InterPro; IPR001304; Lectin_C.
 CC InterPro; IPR000538; Link.
 CC InterPro; IPR003324; SGXSG.
 CC InterPro; IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00008; EGF; 1.
 CC Pfam; PF00047; ig; 1.
 CC Pfam; PF00059; lectin_c; 1.
 CC Pfam; PF02339; SGXSG; 56.
 CC Pfam; PF00084; sushi; 1.
 CC Pfam; PF00193; Xlink; 4.
 CC PRINTS; P00356; ANTIFREEZEII.
 CC PRINTS; P01265; LINKMODULE.
 CC ProDom; PD000918; Link; 4.
 CC SMART; SM00032; CCP; 1.
 CC SMART; SM00034; CLECT; 1.
 CC SMART; SM00179; EGF_CA; 1.
 CC SMART; SM00409; IG; 1.
 CC SMART; SM00445; LINK; 4.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS00026; EGF_3; 1.
 CC PROSITE; PS00187; EGF_CA; 1.
 CC PROSITE; PS00835; IG_LINK; 1.
 CC PROSITE; PS01241; LINK; 4.
 CC Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
 CC Alternative splicing; Repeat; Immunoglobulin domain.
 CC SIGNAL; 1 16
 CC CHAIN; 17 2109
 CC DOMAIN; 34 143
 CC DOMAIN; 166 243
 CC DOMAIN; 264 346
 CC DOMAIN; 537 614
 CC DOMAIN; 635 716
 CC DOMAIN; 1363 1742
 CC 19 X 20 AA TANDEM-REPEAT.

FT	DOMAIN	1855	1892	EGF-LIKE.
FT	DOMAIN	1901	2019	C-TYPE LECTIN.
FT	DOMAIN	2023	2081	SUSHI.
FT	DOMAIN	48	137	G1-A.
FT	DOMAIN	148	243	G1-B.
FT	DOMAIN	249	346	G1-B'.
FT	DOMAIN	519	613	G2-B.
FT	DOMAIN	620	715	G2-B'.
FT	DOMAIN	718	803	KS.
FT	DOMAIN	805	1264	CS-1.
FT	DOMAIN	1265	1742	CS-2.
FT	DOMAIN	1893	2109	G3.
FT	DISULFID	51	129	BY SIMILARITY.
FT	DISULFID	171	242	BY SIMILARITY.
FT	DISULFID	195	216	BY SIMILARITY.
FT	DISULFID	269	345	BY SIMILARITY.
FT	DISULFID	293	314	BY SIMILARITY.
FT	DISULFID	542	613	BY SIMILARITY.
FT	DISULFID	566	587	BY SIMILARITY.
FT	DISULFID	640	715	BY SIMILARITY.
FT	DISULFID	664	685	BY SIMILARITY.
FT	DISULFID	1859	1870	BY SIMILARITY.
FT	DISULFID	1864	1879	BY SIMILARITY.
FT	DISULFID	1881	1890	BY SIMILARITY.
FT	DISULFID	1897	1908	BY SIMILARITY.
FT	DISULFID	1925	2017	BY SIMILARITY.
FT	DISULFID	1993	2009	BY SIMILARITY.
FT	DISULFID	2024	2067	BY SIMILARITY.
FT	DISULFID	2053	2080	BY SIMILARITY.
FT	CARBOHYD	76	76	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	122	122	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	388	388	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	644	644	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	700	700	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	765	765	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	801	801	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPIC	1856	1892	Missing (in isoform 2).
FT	CONFLICT	362	362	/FTid=VSP_003073.
FT	CONFLICT	362	362	E -> D (IN REF. 3).
Query Match 13.3%; Score 146; DB 1; Length 2109;				
Best Local Similarity 25.0%; Pred. No. 8.5e-05;				
Matches 42; Conservative 28; Mismatches 58; Indels 40; Gaps 8;				
Qy	14	QRCYKVIYFDTERRLNFEAKACRDGGQLVSISEDEOKLIEFIENLLPSDGF-	72	
Db	1905	QGHCYR--HFEE---RETWDAESRCRHHQHLSSIIITPEEQEFVNSHAQ-----DYQ	1952	
Qy	73	WIGLRREEKQNSTACODLYATDGSISQFRNMYVDEPS----CGSEVCVMYHQPSAP	128	
Db	1953	WIGLSDR-----AVENDFRSDGHSLOFENWRPNQPDNPFAGEDCVVMWHEQG--	2002	
Qy	129	AGIGGPNYFQNDRCNNKNNFKYIS----DEKPAVPSRAEGEETE	172	
Db	2003	-----EWNVPFCNVHLPTCKGTGACGDPVVENARTFGRKID	2041	

Search completed: September 9, 2004, 22:54:13
Job time : 16.9631 secs

Blank Sheet

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:48:35 ; Search time 24.9386 Seconds
(without alignments)
782.999 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227

Perfect score: 1100

Sequence: 1 RLLSGQPVCRGGRPCYK.....EEDAKTKFKESREALNLAY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	182	16.5	1456	1 A36563	mannose receptor p
2	178.5	16.2	1455	1 A48925	mannose receptor p
3	177	16.1	1268	2 S52791	neurocan - mouse
4	174.5	15.9	1643	2 T14274	versican precursor
5	174.5	15.9	3381	2 T42329	versican precursor
6	174	15.8	1257	2 S28784	neurocan precursor
7	174	15.8	2397	1 A55535	versican precursor
8	174	15.8	2409	1 A60979	versican precursor
9	171	15.5	3562	2 A47171	chondroitin sulfat
10	170.5	15.5	1479	2 T42710	mannose receptor,
11	159.5	14.4	1340	2 A39808	proteoglycan core
12	159.5	14.4	2327	2 T42630	aggreacan - bovine
13	158.5	14.4	2415	1 A39086	aggreacan precursor
14	154.5	14.0	612	2 B42755	E-selectin precurs
15	153.5	14.0	2124	2 A28452	proteoglycan core
16	152	13.8	912	2 A24423	brevican precursor
17	149.5	13.6	459	2 T24425	hypothetical prote
18	149	13.5	321	1 LNHUR	IgE Fc receptor II
19	148.5	13.5	330	2 T46286	brevican - human (
20	148	13.5	253	2 E89130	protein F52E1.2 [1
21	147.5	13.4	2132	1 A55182	aggreacan precursor
22	147	13.4	883	2 S57653	brevican precursor
23	146.5	13.3	162	1 LNRCL	lectin BRA3-1 prec
24	146	13.3	2109	1 I50421	aggreacan precursor
25	145.5	13.2	742	2 JCT595	scavenger receptor
26	145	13.2	883	2 S49126	brevican precursor
27	144.5	13.1	173	2 S10548	lectin - barnacle
28	144.5	13.1	372	2 S23936	L-selectin precurs
29	144.5	13.1	404	2 A46274	HIV gp120-binding

30 143.5 13.0 129 2 JC4329
31 143.5 13.0 372 1 A32375
32 143.5 13.0 463 2 T28655
33 142.5 13.0 131 2 JC5058
34 142 12.9 1487 2 S48719
35 141.5 12.9 331 1 LNMSE
36 140.5 12.8 162 1 LNRCL
37 140 12.7 370 2 S22124
38 139 12.6 248 1 LNHUP5
39 139 12.6 248 1 LNHUP6
40 139 12.6 248 1 LNHUP1
41 139 12.6 283 1 LNFHLS
42 138.5 12.6 152 2 JC4690
43 138.5 12.6 202 2 JC4031
44 138 12.5 280 2 T29200
45 137.5 12.5 309 1 S34198

ALIGNMENTS

RESULT 1

A36563
mannose receptor precursor - human

C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C;Accession: A36563; A60926; A44255; B44255; C44255; D44255; F44255; G44255; H44
R;Taylor, M.E.; Conary, J.T.; Lennartz, M.R.; Stahl, P.D.; Drickamer, K.
J. Biol. Chem. 265, 12156-12162, 1990
A;Title: Primary structure of the mannose receptor contains multiple motifs resembling c
A;Reference number: A36563; MUID:90324192; PMID:2373685
A;Accession: A36563
A;Molecule type: mRNA
A;Residues: 1-1456 <TAY>
A;Cross-references: GB:J05550; NID:G188675; PIDN:AAAS9868.1; PID:G188676
A;Note: Parts of this sequence, including the amino end of the mature protein, were conf
R;Zekowitz, R.A.B.; Sastry, K.; Bailly, P.; Warner, A.
J. Exp. Med. 172, 1785-1794, 1990
A;Title: Molecular characterization of the human macrophage mannose receptor: demonstrat
A;Reference number: A60926; MUID:91079783; PMID:2258707
A;Accession: A60926
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1333, T, 1335-1456 <EZE>
A;Cross-references: GB:X58635
A;Note: translation of the nucleotide sequence is incomplete
A;Note: in the authors' translation additional residues Pro-Glu-Ile are shown after 497-
R;Kim, S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.
Genomics 14, 721-727, 1992
A;Title: Organization of the gene encoding the human macrophage mannose receptor (MRC1).
A;Reference number: A44255; MUID:93052405; PMID:1294118
A;Accession: A44255
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 155-233, 'KSAI', 238-283;346-428;492-569;631-714,716-719;783-820,'N',822-865;'
A;Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:118428,
C;Genetics:
A;Gene: GDB:MRC1
A;Cross-references: GDB:133759; OMIM:153618
A;Map position: 10p13-10p13
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C;Keywords: duplication; lectin; tandem repeat; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;168-209/Domain: fibronectin type II repeat homology <2F1>
F;223-340/Domain: C-type lectin homology <LCHI>
F;362-486/Domain: C-type lectin homology <LCH2>
F;945-1079/Domain: C-type lectin homology <LCH3>

Query Match 16.5%; Score 182; DB 1; Length 1456;

Best Local Similarity 25.5%; Pred. No. 8.3e-08;
Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;

QY .18 YKVIYFHDTSRLNFEAKACRRDGGQLVSISEDEQKLEKFIENLLPDSQDFWIGLR 77

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Db 807 YKDYQYFSEKKEITMDNARAFCKNFGLVSIQSESEKFLWKVY-NRNDQAQSAFYFGLL 865
QY 78 RREKQSNSTACQDIYAWTDSISQFRNYYVDEBSCGS--EVCVVMYHQSPAGIGGPY 135
Db 866 ISLDKX-----FAMWGSKVDYVSWATGEFNANEDENCVTMY-----SNSGF----- 908
QY 136 MFQWDDRCNNKNNFICKYSDEK-----PAVPSREAGBETELTTPVLPEETQE----- 184
Db 909 ---WNDINGVFNAFICQHNSSINATVMP-----TWPSVPSCKEGWNFYSN 954
QY 185 -----EDAKTFKESREAAAL 199
Db 955 KCFKIFGFMERKNQWQBARACI 978

RESULT 2
A48925
mannose receptor precursor, macrophage - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48925; S21320; PC2245
R:Harris, N.; Super, M.; Rits, M.; Chang, G.; Ezekowitz, R.A.
Blood 80, 2363-2373, 1992
A:Title: Characterization of the murine macrophage mannose receptor: demonstration that
A:Reference number: A48925; MUID:93043353; PMID:1421407
A:Accession: A48925
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1455 <HAR>
A:Experimental source: peritoneal macrophage
A>Note: sequence extracted from NCBI backbone (NCBIP:118733)
R:Harris, N.; Super, M.; Rits, M.; Chang, G.; Ezekowitz, R.B.
submitted to the EMBL Data Library, April 1992
A:Description: Characterization of the murine macrophage mannose receptor: Demonstration
on.
A:Reference number: S21320
A:Accession: S21320
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-302, 'W', 303-1117, 'E', 1119-1455 <HAR2>
A:Cross-references: EMBL:Z11974; NID:G52997; PIDN:CAA78028.1; PID:G52998
R:Harris, N.; Peters, L.L.; Eicher, E.M.; Rits, M.; Rasperry, D.; Eichbaum, Q.G.; Super
Biochem. Biophys. Res. Commun. 198, 682-692, 1994
A:Title: The exon-intron structure and chromosomal localization of the mouse macrophage
A:Reference number: PC2245; MUID:94128116; PMID:8297379
A:Accession: PC2245
A:Molecule type: mRNA
A:Residues: 35-105 <HAR3>
C:Genetics:
A:Gene: Mrc1
A:Map position: 2
C:Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C:Keywords: membrane protein; receptor
F:168-209/Domain: fibronectin type II repeat homology <F9>
F:361-485/Domain: C-type lectin homology <LCH1>
F:943-1077/Domain: C-type lectin homology <LCH2>

Query Match 16.2%; Score 178.5; DB 1; Length 1455;
Best Local Similarity 25.9%; Pred. No. 1.7e-07;
Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;

QY 18 YKVYFHTSRLNPFEEAKACRRDGGQLVSIQSEDEKQKLEFIENLLPSDGFNIGLR 77
Db 806 YKDYQYFSEKKEITMDNARAFCKNFGLVSIQSESEKFLWKVY-NKNGQSQPYFGLM 864
QY 78 RREKQSNSTACQDIYAWTDSISQFRNYYVDEBSCGS--EVCVVMYHQSPAGIGGPY 135
Db 865 ISMDKK-----FIWMDGSKVDYVSWATGEFNANEDENCVTMY-----TNSGF----- 907
QY 136 MFQWDDRCNNKNNFICK--YSDEKAVPSREAGBETELTTPVLPEETQE----- 184
Db 908 ---WNDINGVFNAFICQHNSSINATAMP-----TPTTGGCKEGHLYKNK 953

```

```

QY 185 -----EDAKTFKESREAAALN 201
Db 954 CFKIFGFANEEKSWQDAEQACKGL 978

RESULT 3
S52781
neurocan - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-feb-2000
C:Accession: S52781
R:Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, February 1995
A:Description: Amino acid sequence of mouse neurocan and brevicin and their different ex
A:Reference number: S52781
A:Accession: S52781
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1268 <RAU>
A:Cross-references: EMBL:X84727; NID:G758629; PIDN:CAA59216.1; PID:G758630
C:Superfamily: aggregan; C-type lectin homology; complement factor H repeat homology; EGI
F:176-253/Domain: link protein repeat homology <LNK1>
F:274-355/Domain: link protein repeat homology <LNK2>
F:964-995/Domain: EGF homology <EGF>
F:1040-1160/Domain: C-type lectin homology <LCH>
F:1167-1223/Domain: complement factor H repeat homology <FHD>

Query Match 16.1%; Score 177; DB 2; Length 1268;
Best Local Similarity 31.5%; Pred. No. 2e-07;
Matches 45; Conservative 17; Mismatches 49; Indels 32; Gaps 6;

QY 14 QRPCKVYFHTSRLNPFEEAKACRRDGGQLVSIQSEDEKQKLEFIENLLPSDGFN 73
Db 1048 QGHCYK--YF---AHRRAWEDAECDRCRRAGHLTSVHSPEEHKFINSP-----GHENSW 1096

QY 74 IGLRREKQSNSTACQDIYAWTDSISQFRNYYVDEPS---CGSEVCVVMYHQSPAPAG 130
Db 1097 IGLNDRTVED-----FQWTDNTGLQYENWRKQPDNFFAGGDCVVMVAHESG--- 1145

QY 131 IGGPYMFQWDDRCNNKNNFICK 153
Db 1146 -----RWNDVPCNNLPYVCK 1161

RESULT 4
T14274
versican precursor, splice form V2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C:Accession: T14274
R:Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 15758-15764, 1998
A:Title: Versican V2 is a major extracellular matrix component of the mature bovine brain
A:Reference number: Z17954; MUID:98288320; PMID:9624174
A:Accession: T14274
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1643 <SCH>
A:Cross-references: EMBL:AF060458; NID:G3253303; PID:G3253304; PIDN:AAC24360.1
A:Experimental source: brain
C:Keywords: glycoprotein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-1643/Product: versican, splice form V2 #status predicted <MAT>
F:57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 15.9%; Score 174.5; DB 2; Length 1643;
Best Local Similarity 25.5%; Pred. No. 4.4e-07;
Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;

QY 14 QRPCKVYFHTSRLNPFEEAKACRRDGGQLVSIQSEDEKQKLEFIENLLPSDGFN 72
Db 1424 QGQCYK--YF---AHRRTWDAARECRLLQGAHLTSILSHEEQMFVNRV-----GHQYQ 1471

```


[illegible]

RESULT 8
A60979
N/Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
N/Contains: glial hyaluronate-binding protein
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C/Accession: S06014; S43921; A60979; A30358; A29348; A45131; I54179
R/Zimmermann, D.R.; Ruoslahti, E.
EMBO J. 8, 2975-2981, 1989
A/Title: Multiple domains of the large fibroblast proteoglycan, versican.
A/Reference number: S06014; MUID:90059882; PMID:2583089
A/Accession: S06014
A/Molecule type: mRNA
A/Residues: 1-2409 <ZIM>
A/Cross-references: GB:X15998; NID:g37662; PIDN:CAA34128.1; PID:g37663
R/Yao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
A/Title: Identification of the proteoglycan versican in aorta and smooth muscle cells by
A/Reference number: S43921; MUID:95005762; PMID:7921538
A/Accession: S43921
A/Molecule type: mRNA
A/Residues: 208-440;1094-1385;1910-2246 <YAO>
R/Bignami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
Brain Res. Bull. 22, 67-70, 1989
A/Title: Structural similarity of hyaluronate binding proteins in brain and cartilage.
A/Reference number: A60979; MUID:89229983; PMID:2469524
A/Accession: A60979
A/Molecule type: protein
A/Residues: 171-210;289-303 <BIG>
R/Perides, G.; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
J. Biol. Chem. 264, 5981-5987, 1989
A/Title: Isolation and partial characterization of a glial hyaluronate-binding protein.
A/Reference number: A30358; MUID:89174663; PMID:2466833
A/Accession: A30358
A/Molecule type: protein
A/Residues: 24-50;80-87;D',89-119;128-155;167-218;229-259;IR',261-269;277-283,'G',285-
R/Krusius, T.; Gehlsen, K.R.; Ruoslahti, E.
J. Biol. Chem. 262, 13120-13125, 1987
A/Title: A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like
A/Reference number: A29348; MUID:88007514; PMID:2820964
A/Accession: A29348
A/Molecule type: mRNA
A/Residues: 1725,'V',1727-2409 <KR>
A/Cross-references: GB:J02814
R/Perides, G.; Rahemtulla, F.; Lane, W.S.; Asher, R.A.; Bignami, A.
J. Biol. Chem. 267, 23883-23887, 1992
A/Title: Isolation of a large aggregating proteoglycan from human brain.
A/Reference number: A45131; MUID:93054750; PMID:1429726
A/Contents: brain
A/Accession: A45131
A/Molecule type: protein
A/Residues: 21-22,'X',24-37 <PE2>
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBIP:118884)
R/Iozzo, R.V.; Naso, M.F.; Cannizzaro, L.A.; Waemuth, J.J.; McPherson, J.D.
Genomics 14, 845-851, 1992
A/Title: Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chr4
A/Reference number: I54179; MUID:93122792; PMID:1478664
A/Accession: I54179
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 251-347 <RES>
A/Cross-references: GB:S52488; NID:g263313; PIDN:AAB24878.1; PID:g263314
C/Genetics:
A/Gene: GDB:CSPG2
A/Cross-references: GDB:127873; OMIM:118661
A/Map position: 5q12-q14
C/Superfamily: versican; C-type lectin homology; complement factor H repeat homology; EG
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-2409/Product: proteoglycan 24K core protein #status predicted <MAT>
F:167-244/Domain: link protein repeat homology <LNK1>

F:265-346/Domain: link protein repeat homology <LNK2>
F:559-1654/Domain: chondroitin sulfate attachment #status predicted <GAG>
F:2106-2137/Domain: EGF homology <EG1>
F:2144-2175/Domain: EGF homology <EG2>
F:2182-2302/Domain: C-type lectin homology <LCH>
F:2309-2365/Domain: complement factor H repeat homology <FHD>
Query Match 15.8%; Score 174; DB 1; Length 2409;
Best Local Similarity 28.5%; Pred. No. 7.6e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
QY 14 QRPCKVIYFHDTSRLNPEEAKACRRDGGQLVSISEDEQKLEKFIENLLPSDGF- 72
Db 2190 QGQCYK--YF---AHRRTWDAARECRLLQGAHLTSLSHEEQMFVNRV-----GHDYQ 2237
QY 73 WIGLRRREKQSNSTACQDLYAWTDGSIQFNWVDEP-----SCGSEVCVVMYHQPSPAP 128
Db 2238 WIGL-----NDKMFEDFRWTDGSLQYENWRPNQDFFSAGEDCVVIWHENG-- 2287
QY 129 AGIGGPFYMFQWDDRCNMKNPFICKYS-----DEKPAVPSREAEGE 169
Db 2288 -----QWNDVPCNHYLTYTCKGTVACGQPPVVENAKTFGK 2323
RESULT 9
A47171
chondroitin sulfate proteoglycan PG-M core protein - chicken
C/Species: Gallus gallus (chicken)
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C/Accession: A47171
R/Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A/Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during
A/Reference number: A47171; MUID:93300846; PMID:8314802
A/Accession: A47171
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-3562 <SHI>
A/Cross-references: GB:D13542; NID:g391643; PIDN:BAA02742.1; PID:g391644
A/Experimental source: stage 22-23 developing limb buds
A/Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
C/Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin
F:166-243/Domain: link protein repeat homology <LNK1>
F:166-243/Domain: link protein repeat homology <LNK2>
F:3258-3289/Domain: EGF homology <EGF1>
F:3296-3327/Domain: EGF homology <EGF>
F:3334-3454/Domain: C-type lectin homology <LCH>
F:3461-3517/Domain: complement factor H repeat homology <FHD>
Query Match 15.5%; Score 171; DB 2; Length 3562;
Best Local Similarity 28.5%; Pred. No. 2.2e-06;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
QY 14 QRPCKVIYFHDTSRLNPEEAKACRRDGGQLVSISEDEQKLEKFIENLLPSDGF- 72
Db 3342 QGQCYK--YF---AHRRTWDAARECRLLQGAHLTSLSHEEQMFVNRV-----GHDYQ 3389
QY 73 WIGLRRREKQSNSTACQDLYAWTDGSIQFNWVDEP-----SCGSEVCVVMYHQPSPAP 128
Db 3390 WIGL-----NDKMFEDFRWTDGSLQYENWRPNQDFFSAGEDCVVIWHENG-- 3439
QY 129 AGIGGPFYMFQWDDRCNMKNPFICKYS-----DEKPAVPSREAEGE 169
Db 3440 -----QWNDVPCNHYLTYTCKGTVACGQPPVVENAKTFGK 3475
RESULT 10
T42710
mannose receptor, macrophage - mouse
N/Alternate names: lambda lectin; phospholipase A2 receptor
C/Species: Mus musculus (house mouse)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000

C;Accession: T42710
 R;Wu, K.; Yuan, J.; Lasky, L.A.
 J. Biol. Chem. 271, 21323-21330, 1996
 A;Title: Characterization of a novel member of the macrophage mannose receptor type C
 A;Reference number: 222035; MUID:96355501; PMID:8702911
 A;Accession: T42710
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1479 <WUK>
 A;Cross-references: EMBL:U56734; NID:q1336073; PID:q1336074; PIDN:AAC52729.1
 C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
 C;Keywords: membrane protein; receptor
 F;186-227/Domain: fibronectin type II repeat homology <2FR>

Query Match 15.5%; Score 170.5; DB 2; Length 1479;
 Best Local Similarity 31.4%; Pred. No. 8.8e-07;
 Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;

QY 4 SQQVCRGGTQPCYKVIYFHTSRLNFEBAKACRDGGQLVSISEDEQKLEKFI 63
 Db 384 SWQPF-----QGHYRL-----QAKRSWQESKRAKLRGGDLSTHMAELBFTKQIK 433
 QY 64 NLLPSDGDGFWIGLRRREKQSNSTACQDLVAMTDSISQFRNMYVDEPS---CGSEVCVV 120
 Db 434 QEVE---ELMTGL-----NDLKLQNPFWSDGSLVSFTWHPPFPNFRDLEDVCT 482
 QY 121 MYHQPAPAGIGGPFYQWNDRCNMKNFICK 153
 Db 483 IW-----GPEG-----RWNDSPCNQSLPSICK 504

RESULT 11
 A39808
 Proteoglycan core protein, cartilage - bovine (fragments)
 N;Alternate names: aggrecan; aggregating cartilage proteoglycan
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 20-Mar-1992 #sequence revision 23-Mar-1995 #text change 13-Aug-1999
 C;Accession: A34234; A27752; A39808; A27751; E29164; B27751; C27751; E27751; E27
 R;Antonsson, P.; Heinegard, D.; Oldberg, A.
 J. Biol. Chem. 264, 16170-16177, 1989
 A;Title: The keratan sulfate-enriched region of bovine cartilage proteoglycan consists o
 A;Reference number: A34234; MUID:89380219; PMID:2528543
 A;Accession: A34234
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 128-621 <ANT>
 A;Cross-references: GB:J05028
 R;Oldberg, A.; Antonsson, P.; Heinegard, D.
 Biochem. J. 243, 255-259, 1987
 A;Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a
 A;Reference number: A27752; MUID:87270630; PMID:3111460
 A;Accession: A27752
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 622-1340 <OLD>
 R;Sandy, J.D.; Boynton, R.E.; Flannery, C.R.
 J. Biol. Chem. 266, 8198-8205, 1991
 A;Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation of
 A;Reference number: A39808; MUID:91217051; PMID:2022637
 A;Accession: A39808
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-28;59-82;131-137;174-175;177-204;208-225 <PER>
 R;Perin, J.P.; Bonnet, F.; Jolles, P.
 FEBS Lett. 206, 73-77, 1986
 A;Title: Structural relationship between link proteins and proteoglycan monomers.
 A;Reference number: A27751; MUID:87005253; PMID:3530809
 A;Accession: A27751
 A;Molecule type: protein
 A;Residues: 23-58;74-130;174-175;177-204;208-225 <PER>
 R;Perin, J.P.; Bonnet, F.; Jolles, P.
 FEBS Lett. 176, 37-42, 1984
 A;Title: Sequence data concerning the protein core of the cartilage proteoglycan monomer

A;Reference number: A91327; MUID:85027710; PMID:6489519
 A;Accession: E29164
 A;Molecule type: protein
 A;Residues: 1230-1249 <PE2>
 C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
 C;Keywords: glycoprotein
 F;8-28/Domain: link protein repeat homology (fragment) <LNK1>
 F;29-58/Domain: link protein repeat homology (fragment) <LNK2>
 F;80-146/Domain: link protein repeat homology (fragments) <LNK3>
 F;167-248/Domain: link protein repeat homology <LNK4>
 F;1130-1250/Domain: C-type lectin homology <LCH>
 F;1257-1313/Domain: complement factor H repeat homology <FHD>

Query Match 14.4%; Score 158.5; DB 2; Length 1340;
 Best Local Similarity 26.8%; Pred. No. 9.1e-06;
 Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;

QY 6 QPVCRRG---TORPCYKVIYFHTSRLNFEBAKACRDGGQLVSISEDEQKLEKFI 62
 Db 1127 QKLCEGWTKFQGHYR---HFPPD---RATVDAESQCRKQSHLSIVTPEQ-----EFV 1177
 QY 63 ENLLPSDGDGFWIGLRRREKQSNSTACQDLVAMTDSISQFRNMYVDEP-----SCGSEV 117
 Db 1178 NN---NAQDYQWIGL-----NDKTIEGDFRWSGHSLSQFNWRPNQPDNFFATGDC 1226
 QY 118 CVMVYHQPAPAGIGGPFYQWNDRCNMKNFICKYS-----DEKPAYPSRAEGEETE 172
 Db 1227 VVMWHEKG-----EWNVDPVCNQLPFTCKKGTVACGEPVVEHARIFGQKXD 1274

RESULT 12
 T42630
 aggrecan - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 04-Mar-2000
 C;Accession: T42630
 R;Hering, T.M.; Kollar, J.; Huynh, T.D.
 submitted to the EMBL Data Library, September 1996
 A;Description: Complete coding sequence of bovine aggrecan: comparative structural analy
 A;Reference number: Z2182
 A;Accession: T42630
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2327 <HER>
 A;Cross-references: EMBL:U76615; NID:g1730259; PID:g1730260; PIDN:AAB38524.1
 A;Experimental source: articular chondrocytes
 C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
 C;Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprot

Query Match 14.4%; Score 158.5; DB 2; Length 2327;
 Best Local Similarity 26.8%; Pred. No. 1.7e-05;
 Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;

QY 6 QPVCRRG---TORPCYKVIYFHTSRLNFEBAKACRDGGQLVSISEDEQKLEKFI 62
 Db 2114 QKLCEGWTKFQGHYR---HFPPD---RATVDAESQCRKQSHLSIVTPEQ-----BFV 2164
 QY 63 ENLLPSDGDGFWIGLRRREKQSNSTACQDLVAMTDSISQFRNMYVDEP-----SCGSEV 117
 Db 2165 NN---NAQDYQWIGL-----NDKTIEGDFRWSGHSLSQFNWRPNQPDNFFATGDC 2213
 QY 118 CVMVYHQPAPAGIGGPFYQWNDRCNMKNFICKYS-----DEKPAYPSRAEGEETE 172
 Db 2214 VVMWHEKG-----EWNVDPVCNQLPFTCKKGTVACGEPVVEHARIFGQKXD 2261

RESULT 13
 A39086
 aggrecan precursor, cartilage long splice form [validated] - human
 N;Alternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; p
 C;Contains: aggrecan cartilage short splice form
 C;Species: Homo sapiens (man)
 C;Date: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000

C;Accession: A39086; S50206; A43919; S46559; S66389; S68646; S62786; A34226; B43919; C43
 J;Doerge, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
 J. Biol. Chem. 266, 894-902, 1991
 A;Title: Complete coding sequence and deduced primary structure of the human cartilage 1
 A;Reference number: A39086; MUID: 91093289; PMID:1985970
 A;Accession: A39086
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-2162, 2201-2329, 'A', 2392-2415 <DOE>
 A;Cross-references: GB:M55172; NID:G178258; PIDN:AAA62824.1; PID:G178259
 R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
 Biochim. Biophys. Acta 1219, 613-622, 1994
 A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by
 A;Reference number: S50206; MUID: 95035091; PMID:7524681
 A;Accession: S50206
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 350-497 <GLU>
 A;Cross-references: EMBL:X80278; NID:9516295
 A;Note: this translation is not annotated in GenBank entry HSAGGREG, release 113.0
 R;Sandy, J.D.; Flannery, C.R.; Neame, P.U.; Lohmander, L.S.
 J. Clin. Invest. 89, 1512-1516, 1992
 A;Title: The structure of aggrecan fragments in human synovial fluid. Evidence for the
 domain.
 A;Reference number: A43919; MUID: 92235266; PMID:1569188
 A;Accession: A43919
 A;Molecule type: protein
 A;Residues: 361-370, 'X', 372-373, 393-399, 'X', 401-407, 'X', 409 <SNA>
 A;Cross-references: PIDN:AA822079.1; PID:G248844; PIDN:AB22077.1; PID:G248842; PIDN:AAE
 A;Experimental source: synovial fluid
 A;Note: sequences modified after extraction from NCBI backbone
 R;Barry, F.P.; Neame, P.J.; Sasse, J.; Pearson, D.
 Matrix Biol. 14, 323-328, 1994
 A;Title: Length variation in the keratan sulfate domain of mammalian aggrecan.
 A;Reference number: 146998; MUID: 95128522; PMID:7827755
 A;Accession: S46659
 A;Molecule type: DNA
 A;Residues: 764-765, 'A', 767-846, 'V', 848-862, 'X', 864 <BAR>
 A;Cross-references: EMBL:S74659; NID:9807127; PIDN:AA60643.1; PID:9807128
 A;Note: the authors translated the codon GAA for residue 803 as Ala and Cyt for residue
 R;Ilic, M.Z.; Mok, M.T.; Williamson, O.D.; Campbell, M.A.; Hughes, C.E.; Handley, C.J.
 Arch. Biochem. Biophys. 322, 22-30, 1995
 A;Title: Catabolism of aggrecan by explant cultures of human articular cartilage in the
 A;Reference number: S66389; MUID: 96004775; PMID:7574678
 A;Accession: S66389
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 17-23, 24, 'X', 26-27, 393-401, 402-403 <ILI>
 R;Fosang, A.J.; Last, K.; Knauper, V.; Murphy, G.; Neame, P.J.
 FEBS Lett. 380, 17-20, 1996
 A;Title: Degradation of cartilage aggrecan by collagenase-3 (MMP-13).
 A;Reference number: S68646; MUID: 96181659; PMID:8603731
 A;Accession: S68646
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 'V', 404-405, 'XX' <POS>
 R;Dudhia, J.; Davidson, C.M.; Wells, T.M.; Vynios, D.H.; Hardingham, T.E.; Bayliss, M.T.
 Biochem. J. 313, 933-940, 1996
 A;Title: Age-related changes in the content of the C-terminal region of aggrecan in huma
 A;Reference number: S62786; MUID: 96190740; PMID:8611178
 A;Accession: S62786
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1778-1927, 'A', 1929-1963, 'V', 1965-2162, 2201-2415 <DUD>
 A;Cross-references: EMBL:X17406; NID:G30248; PIDN:CAA5463.1; PID:G30249
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1990
 R;Baldwin, C.T.; Reginato, A.M.; Prockop, D.J.
 J. Biol. Chem. 264, 15747-15750, 1989
 A;Title: A new epidermal growth factor-like domain in the human core protein for the lar
 A;Reference number: A34226; MUID: 89380154; PMID:2789216
 A;Accession: A34226
 A;Molecule type: mRNA
 A;Residues: 1936-1963, 'V', 1965-2069, 'A', 2071-2415 <BAL>

A;Cross-references: GB:J05062; NID:G181167; PIDN:AAA35726.1; PID:G181168
 C;Genetics:
 A;Gene: GDB:AGCL; CSPG1; CSPGCP; MSK15
 A;Cross-references: GDB:I27479; OMIM:155760
 A;Map position: 15q26-15q26
 C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF
 C;Keywords: alternative splicing; cartilage; chondroitin sulfate proteoglycan; extracellu
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-2415/Product: aggrecan cartilage long splice form #status predicted <MATL>
 F:20-2162, 2201-2415/Product: aggrecan cartilage short splice form #status predicted <MATL>
 F:20-2162, 2201-2329, 'A', 2392-2415/Product: aggrecan short splice form #status predicted <MATL>
 F:44-135/Domain: immunoglobulin homology <IMM>
 F:170-247/Domain: link protein repeat homology <LNK1>
 F:268-349/Domain: link protein repeat homology <LNK2>
 F:495-572/Domain: link protein repeat homology <LNK3>
 F:593-673/Domain: link protein repeat homology <LNK4>
 F:677-861/Domain: keratan sulfate attachment #status predicted <KSA>
 F:864-1510/Domain: chondroitin sulfate attachment #status predicted <CS1>
 F:1511-2162/Domain: chondroitin sulfate attachment #status predicted <CS2>
 F:2168-2325/Domain: EGF homology <EGF>
 F:2205-2328/Domain: C-type lectin homology <LCH>
 F:2332-2388/Domain: complement factor H repeat homology <FHD>
 F:126, 239, 333, 387, 434, 602, 657, 737, 1898/Binding site: carbohydrate (Asn) (covalent) #statu
 F:371, 376/Binding site: keratan sulfate (Thr) (covalent) #status predicted

Query Match 14.4%; Score 158.5; DB 1; Length 2415;
 Best Local Similarity 29.1%; Pred. No. 1.8e-05;
 Matches 52; Conservative 22; Mismatches 62; Indels 43; Gaps 11;

QY 6 QVCEGG---TORPCYKVIYFHDTSRLNFEAEACRRDGGQVSTSEDEQKLEKFI 62
 DB 2202 QEVCEGKNYQGHYR--HFDP---RETWDACRCRQSHSLSSIVTPEQ---EFV 2252

QY 63 ENLLPSDGF-WIGLRREERQSNSTACQDLYAMTDSISQFRNYYVDEPS---CGSEVC 118
 DB 2253 NN---NAQDYQWIGL-----NDRITGDFRNSDGHQPMQFENWRPNQDNFFAAGBDC 2301

QY 119 VVM-VHQSAPAGIGPGYFQWDRNDRCKNKNFKCKYS---DEKPAVPSREASGETE 172
 DB 2302 VYMIWHEXG-----EWNDVPCNYHLFFCTCKGTACGPFVVEHARTFGQKXD 2349

RESULT 14
 B42755
 E-selectin precursor - mouse
 N;Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1)
 C;Species: Mus musculus (house mouse)
 C;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000 #text_change 02-Aug-2002
 C;Accession: S23174; B42755
 R;Becker-Andre, M.; van Huijsduijnen, R.H.; Losberger, C.; Whelan, J.; Delamarter, J.F.
 Eur. J. Biochem. 206, 401-411, 1992
 A;Title: Murine endothelial leukocyte-adhesion molecule 1 is a close structural and funct
 A;Reference number: S23174; MUID: 92283265; PMID:1375914
 A;Accession: S23174
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-612 <BEC>
 A;Cross-references: GB:M80778; NID:G193014; PIDN:AAA37547.1; PID:G193015
 R;Weller, A.; Isenmann, S.; Vestweber, D.
 J. Biol. Chem. 267, 15176-15183, 1992
 A;Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-selectin
 A;Reference number: A42755; MUID: 92340571; PMID:1378846
 A;Accession: B42755
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 'MKRAGV', 1-389, 391-612 <WEL>
 A;Cross-references: GB:M87862; NID:G193107
 A;Experimental source: endothelial cells
 A;Note: sequence extracted from NCBI backbone (NCBI:109470)
 A;Note: the sequence in GenBank entry MUSELEB, release 117.0, (PIDN:AAA37577.1; PID:G19
 C;Superfamily: P-selectin; C-type lectin homology; complement factor H repeat homology; H
 C;Keywords: glycoprotein; transmembrane protein

F;1-21/Domain: signal sequence #status predicted <SIG>
F;12-138/Domain: C-type lectin homology <LCH>
F;22-612/Product: P-selectin #status predicted <MAT>
F;143-174/Domain: EGF homology <EGF>
F;180-238/Domain: complement factor H repeat homology <FH1>
F;243-300/Domain: complement factor H repeat homology <FH2>
F;305-363/Domain: complement factor H repeat homology <FH3>
F;388-426/Domain: complement factor H repeat homology <FH4>
F;431-489/Domain: complement factor H repeat homology <FH5>
F;494-548/Domain: complement factor H repeat homology <FH6>
F;25,391,528/Binding site: carbohydrate (Asn) #status predicted

Query Match 14.0%; Score 154.5; DB 2; Length 612;
Best Local Similarity 27.9%; Pred. No. 8.3e-06;
Matches 38; Conservative 28; Mismatches 45; Indels 25; Gaps 5;

Qy 22 YHDTSLRLNPFBEAKACRRDGGOLVSISEDEQKLEKFIENLLPSDGFHWGLRRREE 81
Db 23 YYNASSELMTVDEASAYCQRDYTHLVAIQNKEE---INYLNSLNKHSPSYTWIGIRK-- 76

Qy 82 KQSNSTACQDLYAWTDGS---ISQFRNYYVDERS--CGSEVCVMVYHOPSAPAGIGGPYM 136
Db 77 -----VNNVWIIWVGTKPLTEEAQNAQFENKQNRNEDCVETIYIQRDQSGM----- 124

Qy 137 FQWNDRCNMKNFIC 152
Db 125 --WNDERCNKKLALC 138

RESULT 15
A28452
proteoglycan core protein precursor, cartilage - rat
N;Alternate names: aggrecan
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 21-Jan-2000
C;Accession: A92623; A23835; A28453; A28095; A28452
R;Doerge, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 262, 17757-17767, 1987
A;Title: Complete primary structure of the rat cartilage proteoglycan core protein deduced from complementary DNA sequence
A;Reference number: A92623; MUID:88087070; PMID:3693370
A;Accession: A92623
A;Molecule type: mRNA
A;Residues: 1-2124 <DOE>
R;Doerge, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 263, 10040a, 1998
A;Reference number: A30069
C;Contents: annotation; revision to residue 698
R;Doerge, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 261, 8108-8111, 1986
A;Title: Partial cDNA sequence encoding a globular domain at the C terminus of the rat core protein
A;Reference number: A23835; MUID:86250698; PMID:2424893
A;Accession: A23835
A;Molecule type: mRNA
A;Residues: 1856-2124 <DO2>
A;Cross-references: GB:M13518; NID:g206104; PIDN:AAA1836.1; PID:g206105
R;Neame, P.J.; Christner, J.E.; Baker, J.R.
J. Biol. Chem. 262, 17768-17778, 1987
A;Title: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-terminal domain
A;Reference number: A28453; MUID:88087071; PMID:3693371
A;Accession: A28453
A;Molecule type: protein
A;Residues: 20-37,'W',39-60,'E',62-64,'X',66-69,70-83,84,89-148,'L',150-238,'S',240,'A',242-244
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF homology
C;Keywords: Glycoprotein

F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2124/Product: proteoglycan core protein #status predicted <MAT>
F;44-135/Domain: immunoglobulin homology <IMV>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;1914-2034/Domain: C-type lectin homology <LCH>
F;2041-2097/Domain: complement factor H repeat homology <FHD>

F;126,239,333,387,611,667,1842/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.0%; Score 153.5; DB 2; Length 2124;
Best Local Similarity 26.3%; Pred. No. 4.3e-05;
Matches 47; Conservative 27; Mismatches 62; Indels 43; Gaps 9;

Qy 6 QPVCVKG---TORPCVKVIYFHDTSRLNPFBEAKACRRDGGOLVSISEDEQKLEKFI 62
Db 1911 QEQCEGWTKFQGHYR--HFDP---RETWVDAERCREQQSHLSIYTPBEQEFVNKA 1965

Qy 63 ENLLPSDGF--WIGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDERS---SCGEV 117
Db 1966 Q-----DYQWIGL-----NDRITIEGDFWSDGHSLSQPEKWRPNQPNFFATGEDC 2010

Qy 118 CVMVYHOPSAPAGIGGPYMFQWNDRCNMKNFICKYS-----DEKPAVPSREAGEETE 172
Db 2011 VVNIWHERG-----EWNVPCVQLFETCKGTACGEPFAVEHARTLQCKKD 2058

RESULT 16
A54423
brevican precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Sep-1994 #sequence revision 09-Sep-1994 #text_change 21-Jan-2000
C;Accession: A54423; S41914
R;Yamada, H.; Watanabe, K.; Shimonaka, M.; Yamaguchi, Y.
J. Biol. Chem. 269, 10119-10126, 1994
A;Title: Molecular cloning of brevican, a novel brain proteoglycan of the aggrecan/versican family
A;Reference number: A54423; MUID:94193597; PMID:8144512
A;Accession: A54423
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-912 <YAM>
A;Cross-references: GB:X75887; NID:g452820; PIDN:CAA53481.1; PID:g452821
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF homology
F;50-139/Domain: immunoglobulin homology <IMV>
F;174-251/Domain: link protein repeat homology <LNK1>
F;272-353/Domain: link protein repeat homology <LNK2>
F;651-682/Domain: EGF homology <EGF>
F;689-809/Domain: C-type lectin homology <LCH>
F;816-872/Domain: complement factor H repeat homology <FHD>

Query Match 13.8%; Score 152; DB 2; Length 912;
Best Local Similarity 28.8%; Pred. No. 2.2e-05;
Matches 47; Conservative 17; Mismatches 61; Indels 38; Gaps 8;

Qy 14 QRPCVKVIYFHDTSRLNPFBEAKACRRDGGOLVSISEDEQKLEKFIENLLPSDGF 73
Db 697 QGACYK----HFSARR-SWEAEAKRCMYGAHLASISTPEQDFINNRYEQ-----W 745

Qy 74 IGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDERS---CGSEVCVMV-YHQPSADA 129
Db 746 IGL-----NDRITIEGDFLWSDGVPLLYENNPFQDPSYFLSGENCYVMVYHDPDQG--- 794

Qy 130 GIGGPYMFQWNDRCNMKNFICKYS-----DEKPAVPSREAGE 168
Db 795 -----QWSDVPCNYHLISYCKMGLVSCGPPPELPPLAEVFG 829

RESULT 17
T24425
hypothetical protein T04A8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24425
R;Palmer, S.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19889
A;Accession: T24425
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-459 <WIL>
A;Cross-references: EMBL:Z35663; PIDN:CAA84726.1; GSPDB:GN00021; CESP:T04A8.3

A;Molecule type: DNA
A;Residues: 1-253 <STO>
A;Cross-references: GB:chr_V; PIDN:AAB37037.1; PID:gi086809; GSPDB:GNC00023; CESP:F52E1.2
C;Genetics:
A;Gene: F52E1.2
A;Map position: 5

Query Match 13.5%; Score 148; DB 2; Length 253;
Best Local Similarity 29.2%; Pred. No. 1.1e-05;
Matches 49; Conservative 24; Mismatches 57; Indels 38; Gaps 10;

QY 9 CRGG-----TQPCYKV--IYFHDTSRLNFE-----AKEACRRDGGQGLVSI 51
DB 96 CPGGPTGQYVNSKCYKVLHFLHCLSKVQLQKFDAAVYAGATSACAAQAEIVTIDS 155
QY 52 EDEQKLIKFIEN--LLPSDGDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNYYVD 109
DB 156 PDENDALRKAFDTNALVDKTKETWGLK-----SLSGAWQ-----WADGSSATYTNWAPS 205
QY 110 EPGCGSEVCVMYHOPSPAGIGGPMFQ--WDDRCNMKN-NFICK 153
DB 206 QPS-SNGLCVQMITDLSNA---TYKQRGWKTYGCKTSASYICE 248

RESULT 21
A53182
aggrecan precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: A53182; S55329; S50207; S51355; I78532; I58123
R;Walcz, E.; Deak, F.; Erhardt, P.; Coulter, S.N.; Fueloep, C.; Horvath, P.; Doege, K.J.
Genomics 22; 364-371, 1994
A;Title: Complete coding sequence, deduced primary structure, chromosomal localization,
A;Reference number: A53182; MUID:95104847; PMID:7806222
A;Accession: A53182
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-2132 <WAL>
A;Cross-references: GB:I07049; NID:G678541; PIDN:AAC37670.1; PID:gl91772
R;Watanabe, H.; Gao, L.; Sugiyama, S.; Doege, K.; Kimata, K.; Yamada, Y.
Biochem. J. 308, 433-440, 1995
A;Title: Mouse aggrecan, a large cartilage proteoglycan: protein sequence, gene structur
A;Reference number: S55329; MUID:95289972; PMID:7772024
A;Accession: S55329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-567, 'G', 569-1728, 'I', 1730-2132 <WAT1>
A;Cross-references: GB:U22901; NID:G886014
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50207
A;Molecule type: mRNA
A;Residues: 350-481, 'R', 483-506 <GLU1>
A;Cross-references: EMBL:X80279; NID:G673432
R;Glumoff, V.
submitted to the EMBL Data Library, July 1994
A;Reference number: S51355
A;Accession: S51355
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 350-383, 'CPVMSQRRFPAA' <GLU2>
A;Cross-references: EMBL:X80279
R;Watanabe, H.; Kimata, K.; Line, S.; Strong, D.; Gao, L.Y.; Kozak, C.A.; Yamada, Y.
Nature Genet. 7, 154-157, 1994
A;Title: Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in the aggrec
A;Reference number: I58123; MUID:95004579; PMID:7920633
A;Accession: I78532
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 211-326 <WAT2>
A;Cross-references: GB:S73722; NID:G765215; PIDN:AAB32160.1; PID:G765216

Query Match 13.5%; Score 149; DB 1; Length 321;
Best Local Similarity 30.2%; Pred. No. 1.2e-05;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY 14 QPCYKVIYFHTSRRLNFEAKACRRDGGQGLVSISEDEQKLIKFIENLILPSGDFW 73
DB 171 QKCYK---YFGKGTQK--WVHARYACDDMEQGLVSIHSPEDQFLTKH-----ASHTGSW 220
QY 74 IGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPSGGS--EVCVMYHQPSPAGI 131
DB 221 IGLRNLKKE-----FIWVDSHVDYGNWAPGFTSRSGQEDCVMM-----RGS 265
QY 132 GGPTYFQWDDRCNMK--NFTCKYSDEKPAV---PSREARGE-----ETELTPV 177
DB 266 G-----RWDAFCRKLGAWVC-----DLATCTPPASEGSAENGPDRPDGRLPTPS 316
QY 178 LP 179
DB 317 AP 318

RESULT 19
T46256
brevican - human (fragment)
N;Alternate names: protein DKFZp761L191.1
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
C;Accession: T46256
R;Osterweider, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23031
A;Accession: T46256
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-330 <AAA>
A;Cross-references: EMBL:AL137504
A;Experimental source: adult amygdala; clone DKFZp761L191
C;Genetics:
A;Note: DKFZp761L191.1
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; Bg

Query Match 13.5%; Score 148.5; DB 2; Length 330;
Best Local Similarity 29.5%; Pred. No. 1.4e-05;
Matches 46; Conservative 16; Mismatches 57; Indels 37; Gaps 8;

QY 5 GQPCVCGG---TQPCYKVIYFHTSRRLNFEAKACRRDGGQGLVSISEDEQKLIKFI 61
DB 103 GLRFCNPGWDAFQACYK---HFSTR-SWEAEATQCRMYGAHLASTISTPEEQDFINR 157
QY 62 IENLLPSDGDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS---CGSEVC 118
DB 158 YREYQ-----WIGL-----NDRTIEGDFLMSDGVPLLYENWNPQPDYSYFLSGENC 203
QY 119 VVM-YHQPSPAGIGGPMFQWDDRCNMKNFICK 153
DB 204 VVMYHDOG-----QMSDVPCNYHLSYTK 228

RESULT 20
E89130
protein F52E1.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E89130
R;anonymus, The C. elegans Sequencing Consortium.
Science 282, 2012-2019, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: E89130
A;Status: preliminary

Query Match 13.5%; Score 148; DB 2; Length 253;
Best Local Similarity 29.2%; Pred. No. 1.1e-05;
Matches 49; Conservative 24; Mismatches 57; Indels 38; Gaps 10;

QY 9 CRGG-----TQPCYKV--IYFHDTSRLNFE-----AKEACRRDGGQGLVSI 51
DB 96 CPGGPTGQYVNSKCYKVLHFLHCLSKVQLQKFDAAVYAGATSACAAQAEIVTIDS 155
QY 52 EDEQKLIKFIEN--LLPSDGDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNYYVD 109
DB 156 PDENDALRKAFDTNALVDKTKETWGLK-----SLSGAWQ-----WADGSSATYTNWAPS 205
QY 110 EPGCGSEVCVMYHOPSPAGIGGPMFQ--WDDRCNMKN-NFICK 153
DB 206 QPS-SNGLCVQMITDLSNA---TYKQRGWKTYGCKTSASYICE 248

RESULT 21
A53182
aggrecan precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: A53182; S55329; S50207; S51355; I78532; I58123
R;Walcz, E.; Deak, F.; Erhardt, P.; Coulter, S.N.; Fueloep, C.; Horvath, P.; Doege, K.J.
Genomics 22; 364-371, 1994
A;Title: Complete coding sequence, deduced primary structure, chromosomal localization,
A;Reference number: A53182; MUID:95104847; PMID:7806222
A;Accession: A53182
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-2132 <WAL>
A;Cross-references: GB:I07049; NID:G678541; PIDN:AAC37670.1; PID:gl91772
R;Watanabe, H.; Gao, L.; Sugiyama, S.; Doege, K.; Kimata, K.; Yamada, Y.
Biochem. J. 308, 433-440, 1995
A;Title: Mouse aggrecan, a large cartilage proteoglycan: protein sequence, gene structur
A;Reference number: S55329; MUID:95289972; PMID:7772024
A;Accession: S55329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-567, 'G', 569-1728, 'I', 1730-2132 <WAT1>
A;Cross-references: GB:U22901; NID:G886014
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50207
A;Molecule type: mRNA
A;Residues: 350-481, 'R', 483-506 <GLU1>
A;Cross-references: EMBL:X80279; NID:G673432
R;Glumoff, V.
submitted to the EMBL Data Library, July 1994
A;Reference number: S51355
A;Accession: S51355
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 350-383, 'CPVMSQRRFPAA' <GLU2>
A;Cross-references: EMBL:X80279
R;Watanabe, H.; Kimata, K.; Line, S.; Strong, D.; Gao, L.Y.; Kozak, C.A.; Yamada, Y.
Nature Genet. 7, 154-157, 1994
A;Title: Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in the aggrec
A;Reference number: I58123; MUID:95004579; PMID:7920633
A;Accession: I78532
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 211-326 <WAT2>
A;Cross-references: GB:S73722; NID:G765215; PIDN:AAB32160.1; PID:G765216

A:Accession: I58123
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 211-240, 'NCTASLRWRVSRMRHPQRNPSRRQFTS', 'AGGWHAMPQASSTWFGRAVVTCAALAGW', 'R
A:CROSS-references: GB:S73720; NID:G765211; PIDN:AAB32159.1; PID:G765212
C:Genetics:
A:Map position: 7
A:Introns: 253/1
C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC
C:Keywords: cartilage; extracellular matrix
F:1-19/Domain: signal sequence #status predicted <SIG>
F:44-135/Domain: immunoglobulin homology <IMM>
F:170-247/Domain: link protein repeat homology <LNK1>
F:268-345/Domain: link protein repeat homology <LNK2>
F:504-581/Domain: link protein repeat homology <LNK3>
F:602-683/Domain: link protein repeat homology <LNK4>
F:1922-2042/Domain: C-type lectin homology <LCH>
F:2049-2105/Domain: complement factor H repeat homology <FHD>
Query Match 13.4%; Score 147.5; DB 1; Length 2132;
Best Local Similarity 24.7%; Pred. No. 0.00015;
Matches 45; Conservative 30; Mismatches 64; Indels 43; Gaps 9;
QY 3 LSGQVCRGG---TORPCYKVIYFHDTSRRINFEEAKACRRDGGQLVSISEDEQKLE 59
DB 1916 VADQCEGEGWTKFQCHCYR--HFPD---RETWDAERRCRCEQQSHLSIIVTPEEQEFVN 1970
QY 60 KFIENLLPSDGDGFWIGLRREERKQSNSTACQDLIYANTDGSISQFRNMYVDEP-----SCG 114
DB 1971 KNAQ-----DYQWIGU-----NDRTEGFRWSDGHSLOFEXWRPNQDNFFATG 2015
QY 115 SEVCVVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYS-----DKPAPVPSREAE 170
DB 2016 EDCVVMWHERG-----EWNDVPCNYQLPFTCKKGTACVAGDPFVVEHARTLGQK 2064
QY 171 TE 172
DB 2065 KD 2066
RESULT 22
S57653
brevican precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
C:Accession: S57653
R:Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
Submitted to the EMBL Data Library, May 1995
A:Description: Cloning and sequence of mouse neurocan and brevican and their different
A:Reference number: S57653
A:Accession: S57653
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-883 <RAU>
A:CROSS-references: EMBL:X87096; NID:Q886889; PIDN:CAA60575.1; PID:Q886890
C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC
F:49-138/Domain: immunoglobulin homology <IMM>
F:173-250/Domain: link protein repeat homology <LNK1>
F:271-352/Domain: link protein repeat homology <LNK2>
F:626-657/Domain: EGF homology <EGF>
F:664-784/Domain: C-type lectin homology <LCH>
F:791-847/Domain: complement factor H repeat homology <FHD>
Query Match 13.4%; Score 147; DB 2; Length 883;
Best Local Similarity 29.7%; Pred. No. 5.9e-05;
Matches 43; Conservative 21; Mismatches 45; Indels 36; Gaps 8;
QY 14 QRPCYKVIYFHDTSRRINFEEAKACRRDGGQLVSISEDEQKLI-EKFIENLLPSDGDG 72
DB 672 QGACYK---HFSTR-SWEAEQQCRALGNHLSICTPEQDFVNDRYEQ-----719
QY 73 WIGLRREERKQSNSTACQDLIYANTDGSISQFRNMYVDEPS---CGSEVCVVM-YHQPSAP 128

DB 720 WIGL-----NDRTEGDFLWSDGAPLLYENWNPQPDSTYFLSGENCVVMVHMQG-- 769
QY 129 AGIGGPFYMFQWDDRCNMKNFICK 153
DB 770 -----QWSDVPCNVHLSYTK 785
RESULT 23
LNRC1
lectin BRA3-1 precursor - barnacle (Megabalanus rosa)
C:Species: Megabalanus rosa
C:Date: 24-Feb-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C:Accession: JCI503; A26094
R:Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T.
Gene 128, 251-255, 1993
A:Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure and
A:Reference number: JCI503; MUID:93292994; PMID:8514190
A:Accession: JCI503
A:Molecule type: DNA; mRNA
A:Residues: 1-162 <TAK>
A:CROSS-references: DDBJ:D13299
R:Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-295, 1986
A:Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
A:Reference number: A26094
A:Accession: A26094
A:Molecule type: protein
A:Residues: 25-145, 'K', 147-162 <MUR>
A:Note: 146-Arg was also found
C:Comment: This galactose-binding lectin is isolated from the coelomic fluid.
C:Comment: This protein plays important roles in defense mechanisms and in development ar
C:Comment: The molecule is a tetramer of identical chains.
C:Genetics:
A:Introns: 22/1; 47/2; 86/3
A:Superfamily: tetranectin; C-type lectin homology
C:Keywords: hemolymph; homotetramer; lectin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-162/Product: lectin BRA3-1 #status experimental <MAT>
F:26-150/Domain: C-type lectin homology <LCH>
F:26-39, 56-150, 125-142/Disulfide bonds: #status experimental
F:157/Disulfide bonds: interchain (to 160) #status experimental
F:160/Disulfide bonds: interchain (to 157) #status experimental
Query Match 13.3%; Score 146.5; DB 1; Length 162;
Best Local Similarity 25.0%; Pred. No. 9.1e-06;
Matches 40; Conservative 26; Mismatches 59; Indels 35; Gaps 6;
QY 2 LLSGQVCRGGTORPCYKVIYFHDTSRRINFEEAKACR--RDGGQLVSISEDEQKLE 59
DB 19 ITTGCTCGNLWDQYDGHCHCWASTYQVRWMDAQLACQTVHPGAYLATIQSLENAFIS 78
QY 60 KFIENLLPSDGDGFWIGLRREERKQSNSTACQDLIYANTDGSISQFRNMYVDEPS-----C 113
DB 79 ETVSN-----NRLWIGL-----NDIDLEGHVYWSNGEATDFTYWSNNPNWENQDC 125
QY 114 GSEVCVVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICK 153
DB 126 G-----VWVYDVTG-----QWDDDDCCNKNRFLCK 151
RESULT 24
I50421
aggrecan precursor - chicken
N:Alternate names: cartilage chondroitin sulfate proteoglycan core protein
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C:Accession: I50421; S27356; A25442; A32002; I50216; A37072; B37072
R:Li, H.; Schwartz, N.B.; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A:Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
A:Reference number: A48884; MUID:94043149; PMID:8226878
A:Accession: I50421
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-2109 <LIX>
A:Cross-references: GB:I21913; NID:G416133; PIDN:AA19128.1; PID:G416134
R:Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 296, 885-887, 1993
A:Reference number: S39796; MUID:94107258; PMID:8280087
A:Contents: annotation; erratum
A:Accession: S39796
A:Molecule type: mRNA
A:Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1602, 'A'
A:Cross-references: GB:M88101
R:Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 288, 903-910, 1992
A:Title: Molecular cloning of chicken aggrecan. Structural analyses.
A:Reference number: S27356; MUID:93111968; PMID:1339285
A:Accession: S27356
A:Molecule type: mRNA
A:Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1549, 'T'
A:Cross-references: EMBL:M88101
R:Sai, S.; Tanaka, T.; Koshier, R.A.; Tanzer, M.L.
Proc. Natl. Acad. Sci. U.S.A. 83, 5081-5085, 1986
A:Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteoglycan.
A:Reference number: A25442; MUID:86259736; PMID:3460082
A:Accession: A25442
A:Molecule type: mRNA
A:Residues: 1693-1795, 'G', 1797-1855, 1894-2109 <SAI>
A:Cross-references: GB:M13993; NID:G211654; PIDN:AA48720.1; PID:G211655
A:Experimental source: sternal cartilage
R:Tanaka, T.; Har-El, R.; Tanzer, M.L.
J. Biol. Chem. 263, 15831-15835, 1988
A:Title: Partial structure of the gene for chicken cartilage proteoglycan core protein.
A:Reference number: A32002; MUID:89008500; PMID:3170613
A:Accession: A32002
A:Molecule type: DNA
A:Residues: 1893-1987, 'S', 1989-2022 <TAN>
A:Note: The authors translated the codon TCC for residue 1787 as Phe
R:Krueger, R.C.
J. Biol. Chem. 265, 12088-12097, 1990
A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide sequence.
A:Reference number: I50216; MUID:90307744; PMID:1694853
A:Accession: I50216
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'PA', 1044-1559 <KRU>
A:Cross-references: GB:M38187; NID:G211685; PIDN:AAA48731.1; PID:G555441
R:Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.
J. Biol. Chem. 265, 12075-12087, 1990
A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation and characterization of cDNA clones.
A:Reference number: A37072; MUID:90307743; PMID:2365711
A:Accession: A37072
A:Molecule type: protein
A:Residues: 998-1015, 'X', 1017-1019, 'X', 1021-1023 <KR2>
A:Note: amino end of 86K core peptide CS-A
A:Accession: B37072
A:Molecule type: protein
A:Residues: 1247-1250, 'D', 1252-1272, 'X', 1274-1275 <KR3>
A:Note: amino end of 75K core peptide CS-B
C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF repeat homology
C:Keywords: alternative splicing
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-2109/Product: aggrecan #status predicted <WAT>
F:44-131/Domain: immunoglobulin homology <IMM>
F:166-243/Domain: link protein repeat homology <LNK1>
F:264-346/Domain: link protein repeat homology <LNK2>
F:537-614/Domain: link protein repeat homology <LNK3>
F:635-716/Domain: link protein repeat homology <LNK4>
F:1859-1890/Domain: EGF homology <EGF>
F:1897-2017/Domain: C-type lectin homology <LCH>
F:12024-2080/Domain: complement factor H repeat homology <FHD>

Query Match 13.3%; Score 146; DB 1; Length 2109;
Best Local Similarity 25.0%; Pred. No. 0.0002;
Matches 42; Conservative 28; Mismatches 58; Indels 40; Gaps 8;

QY 14 QRPCVKVYFHTSRRLNFEAKACRRDGGQGLYSIESEDEQKLIEXFIENLLPSDGGDF- 72
DB 1905 QGHCYR--HFEE--RRTWMDAESCRHQAHLISITPESQEFVNSHAQ-----DYQ 1952
QY 73 WIGLARREBKQSNSTACQDLVATWDGSIQSFRNMYVDEPS-----CGSEVVMYHQPAP 128
DB 1953 WIGLSDR-----AVENDPWSGHSIQENWRPNQDNFFPAGEDCVVMWHEQG-- 2002
QY 129 AGIGPYMFPQWDDRCNMKNFICKYS-----DEKPAVSREAGETE 172
DB 2003 -----EWNVPNCVHLPTCKGTVACGDPVVENARTFGRKKD 2041

RESULT 25

JC7595

scavenger receptor with C-type lectin type I - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C:Accession: JC7595

R:Nakamura, K.; Funakoshi, H.; Miyamoto, K.; Tokunaga, F.; Nakamura, T.

Biochem. Biophys. Res. Commun. 280, 1028-1035, 2001

A:Title: Molecular cloning and functional characterization of a human scavenger receptor

A:Reference number: JC7595; MUID:21092718; PMID:11162630

A:Contents: Placenta

A:Accession: JC7595

A:Molecule type: mRNA

A:Residues: 1-742 <NAK>

A:Cross-references: DDBJ:AB038518

C:Comment: This receptor, a member of the scavenger receptor family, belonging to the tyrosine kinase receptor subfamily, is involved in the recognition of a ligand and plays an important role in host defense. It forms a trimer and plays a role in recognizing infect

C:Genetics:

A:Gene: srcl-I

A:Map position: 18p11.32

C:Keywords: coiled coil; glycoprotein; transmembrane protein

F:1-39/Domain: cytosolic (amino-terminus) #status predicted <CYT>

F:16-19/Region: internalization signal YKRF

F:40-56/Domain: transmembrane #status predicted <TMM>

F:57-112/Domain: extracellular #status predicted <EXT>

F:113-335/Domain: coiled coil #status predicted <COC>

F:369-384/Region: serine/threonine-rich #status predicted

F:443-589/Domain: collagen-like #status predicted <COL>

F:607-732/Domain: C-type lectin/carbohydrate recognition domain #status predicted <CRD>

Query Match 13.2%; Score 145.5; DB 2; Length 742;

Best Local Similarity 28.7%; Pred. No. 6.5e-05;

Matches 39; Conservative 17; Mismatches 61; Indels 19; Gaps 5;

QY 22 YFHTSRRLNFEAKACRRDGGQGLYSIESEDEQKLIEXFIENLLPSDGGDFWIGLRRRE 81

DB 619 YPFSVEKEI-FEDAKLFCEDKSHLVFINREQQWIKK-----QMVGRSHWIGLTDSE 673

QY 82 QKSNSTACQDLVATWDGSIQSFRNMYVDEPSCGSEVVMYHQPAPAGIGPYMFPQWND 141

DB 674 ENE-----WKWLDGTSFDYKNWKAGQPDNNGH-----GHGPGEDCA-GLIYAGQWND 719

QY 142 DRCMKNFICKYSDE 157

DB 720 FQEDVYNFICEKRE 735

Search completed: September 9, 2004, 22:57:39

Job time : 25.9386 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2004, 22:56:51 ; Search time 90.2776 Seconds
(without alignments)
721.109 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227

Perfect score: 1100

Sequence: 1 RLLSGQPVCRGGTQPCVKY.....EEDAKTFKESREALNLAY 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	100.0	206	9	US-09-887-855-5
2	1100	100.0	374	9	US-09-887-855-2
3	1100	100.0	374	14	US-10-149-819-15
4	1100	100.0	374	15	US-10-094-749-2090
5	1100	100.0	374	15	US-10-264-237-2579
6	1100	100.0	374	16	US-10-648-593-148
7	1100	100.0	387	12	US-10-236-115-1311
8	1096	99.6	374	15	US-10-094-749-2142
9	1090	99.1	374	12	US-10-351-334-166
10	1086	98.7	382	9	US-09-909-320-137
11	1086	98.7	382	9	US-09-909-088B-137
12	1086	98.7	382	9	US-09-905-291A-137
13	1086	98.7	382	9	US-09-902-853-137
14	1086	98.7	382	9	US-09-907-824-137
15	1086	98.7	382	9	US-09-907-841-137

16	1086	98.7	382	10	US-09-904-011-137	Sequence 137, App
17	1086	98.7	382	10	US-09-906-742-137	Sequence 137, App
18	1086	98.7	382	10	US-09-906-838-137	Sequence 137, App
19	1086	98.7	382	10	US-09-907-613-137	Sequence 137, App
20	1086	98.7	382	10	US-09-907-942-137	Sequence 137, App
21	1086	98.7	382	10	US-09-904-859-137	Sequence 137, App
22	1086	98.7	382	10	US-09-909-204-137	Sequence 137, App
23	1086	98.7	382	10	US-09-904-820-137	Sequence 137, App
24	1086	98.7	382	10	US-09-904-786-137	Sequence 137, App
25	1086	98.7	382	10	US-09-906-646-137	Sequence 137, App
26	1086	98.7	382	10	US-09-906-700-137	Sequence 137, App
27	1086	98.7	382	10	US-09-903-786-137	Sequence 137, App
28	1086	98.7	382	10	US-09-903-903-137	Sequence 137, App
29	1086	98.7	382	10	US-09-903-749A-137	Sequence 137, App
30	1086	98.7	382	10	US-09-904-119-137	Sequence 137, App
31	1086	98.7	382	10	US-09-904-956-137	Sequence 137, App
32	1086	98.7	382	10	US-09-902-736-137	Sequence 137, App
33	1086	98.7	382	10	US-09-907-794-137	Sequence 137, App
34	1086	98.7	382	10	US-09-903-943-137	Sequence 137, App
35	1086	98.7	382	10	US-09-904-462-137	Sequence 137, App
36	1086	98.7	382	10	US-09-907-925-137	Sequence 137, App
37	1086	98.7	382	10	US-09-902-692-137	Sequence 137, App
38	1086	98.7	382	10	US-09-903-520-137	Sequence 137, App
39	1086	98.7	382	10	US-09-905-056-137	Sequence 137, App
40	1086	98.7	382	10	US-09-909-064-137	Sequence 137, App
41	1086	98.7	382	10	US-09-904-553-137	Sequence 137, App
42	1086	98.7	382	10	US-09-905-381-137	Sequence 137, App
43	1086	98.7	382	10	US-09-905-088-137	Sequence 137, App
44	1086	98.7	382	10	US-09-907-575-137	Sequence 137, App
45	1086	98.7	382	10	US-09-905-075-137	Sequence 137, App

ALIGNMENTS

RESULT 1
US-09-887-855-5
; Sequence 5: Application US/09887855
; Patent No. US20020059310A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Anderson, Dirk M
; TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
; FILE REFERENCE: 2883-US
; CURRENT APPLICATION NUMBER: US/09/887,855
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-855-5

Query Match 100.0%; Score 1100; DB 9; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-103;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	RLLSGQPVCRGGTQPCVKYVYFHDTSRLNFEAEACRRDGGQLVSISEDEQKLEK	60
Db	4	RLLSGQPVCRGGTQPCVKYVYFHDTSRLNFEAEACRRDGGQLVSISEDEQKLEK	63
Qy	61	FIENLLPSDGDFFWIGLRRREKQSNSTACODLYAWTDGSIQFNNWYVDFPSCGSEVCVV	120
Db	64	FIENLLPSDGDFFWIGLRRREKQSNSTACODLYAWTDGSIQFNNWYVDFPSCGSEVCVV	123
Qy	121	MYIQSPAPAGIGGPFYQWNNDRCNMKNFICKYSEKAPVPSREAGETELTTPVLPE	180
Db	124	MYIQSPAPAGIGGPFYQWNNDRCNMKNFICKYSEKAPVPSREAGETELTTPVLPE	183
Qy	181	ETOEEDAKTKFKESREALNLAY 203	
Db	184	ETOEEDAKTKFKESREALNLAY 206	

RESULT 2

US-09-887-855-2
; Sequence 2, Application US/09887855
; Patent No. US20020058310A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Anderson, Dirk M
; TITLE OF INVENTION: LECTIN S33939 DNA AND POLYPEPTIDES
; FILE REFERENCE: 2883-US
; CURRENT APPLICATION NUMBER: US/09/887,855
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-855-2

Query Match 100.0%; Score 1100; DB 9; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102; Indels 0; Gaps 0;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGQTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSI ESEDEQKLEK 60
DB 25 RLLSGQPVCRGQTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSI ESEDEQKLEK 84
QY 61 FIENLLPSDGFWIGLRREEXQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
DB 85 FIENLLPSDGFWIGLRREEXQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 144
QY 121 MYHQPAPAGIGGPFYFQWDDRCNMKNFICKYSDKPAVPSREAGEETEELTTPVLPE 180
DB 145 MYHQPAPAGIGGPFYFQWDDRCNMKNFICKYSDKPAVPSREAGEETEELTTPVLPE 204
QY 181 ETQEDAKTKFKESREAAINLAY 203
DB 205 ETQEDAKTKFKESREAAINLAY 227

RESULT 3

US-10-149-819-15
; Sequence 15, Application US/10149819
; Publication No. US20030044913A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: AZIMZAI, Valda
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: SHAH, Purvi
; APPLICANT: LAL, Preeti
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PF-0760 PCT
; CURRENT APPLICATION NUMBER: US/10/149,819
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
; PRIOR FILING DATE: 1999-12-10; 1999-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030044913A1 3143411CD1

US-10-149-819-15

Query Match 100.0%; Score 1100; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102; Indels 0; Gaps 0;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGQTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSI ESEDEQKLEK 60
DB 25 RLLSGQPVCRGQTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSI ESEDEQKLEK 84
QY 61 FIENLLPSDGFWIGLRREEXQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
DB 85 FIENLLPSDGFWIGLRREEXQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 144
QY 121 MYHQPAPAGIGGPFYFQWDDRCNMKNFICKYSDKPAVPSREAGEETEELTTPVLPE 180
DB 145 MYHQPAPAGIGGPFYFQWDDRCNMKNFICKYSDKPAVPSREAGEETEELTTPVLPE 204
QY 181 ETQEDAKTKFKESREAAINLAY 203
DB 205 ETQEDAKTKFKESREAAINLAY 227

RESULT 4

US-10-094-749-2090
; Sequence 2090, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAL, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAWATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NACHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2090
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2090

Query Match 100.0%; Score 1100; DB 15; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGQTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSI ESEDEQKLEK 60
DB 25 RLLSGQPVCRGQTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSI ESEDEQKLEK 84
QY 61 FIENLLPSDGFWIGLRREEXQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
DB 85 FIENLLPSDGFWIGLRREEXQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 144

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204
QY 181 ETQEDAKKTFKESREAAALNAY 203
Db 205 ETQEDAKKTFKESREAAALNAY 227

RESULT 5
US-10-264-237-2579
; Sequence 2579, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birtse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2976
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2579
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2579

Query Match 100.0%; Score 1100; DB 15; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIK 60
Db 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIK 84

QY 61 FIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 120
Db 85 FIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 144

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204

QY 181 ETQEDAKKTFKESREAAALNAY 203
Db 205 ETQEDAKKTFKESREAAALNAY 227

RESULT 6
US-10-648-593-148
; Sequence 148, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204

QY 181 ETQEDAKKTFKESREAAALNAY 203
Db 205 ETQEDAKKTFKESREAAALNAY 227

RESULT 7
US-10-296-115-1311
; Sequence 1311, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1311
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1311

Query Match 100.0%; Score 1100; DB 12; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.5e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIK 60
Db 38 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIK 97

QY 61 FIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 120
Db 98 FIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 157

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 158 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 217

QY 181 ETQEDAKKTFKESREAAALNAY 203
Db 218 ETQEDAKKTFKESREAAALNAY 240

RESULT 8
US-10-094-749-2142
; Sequence 2142, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI

US-10-648-593-148

Query Match 100.0%; Score 1100; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIK 60
Db 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIK 84

QY 61 FIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 120
Db 85 FIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 144

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204

QY 181 ETQEDAKKTFKESREAAALNAY 203
Db 205 ETQEDAKKTFKESREAAALNAY 227

RESULT 7
US-10-296-115-1311
; Sequence 1311, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1311
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1311

Query Match 100.0%; Score 1100; DB 12; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.5e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIK 60
Db 38 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIK 97

QY 61 FIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 120
Db 98 FIENLLPSDGFHWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPSCGSEVCV 157

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 158 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 217

QY 181 ETQEDAKKTFKESREAAALNAY 203
Db 218 ETQEDAKKTFKESREAAALNAY 240

RESULT 8
US-10-094-749-2142
; Sequence 2142, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI

```

; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIC, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2142
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-094-749-2142

Query Match          99.6%; Score 1096; DB 15; Length 374;
Best Local Similarity 99.5%; Pred. No. 3.6e-102;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLLSGQVPCRGGTQPCVKIYFHDTSRRLNFEEAKACRRDGGQLVSEDEQKLIK 60
Db 25 RLLSGQVPCRGGTQPCVKIYFHDTSRRLNFEEAKACRRDGGQLVSEDEQKLIK 84

Qy 61 FIENLLPSDGFWIGLRREKQSNSTACQDLVATDGSISQFRNWXVDEPSCGSEVCV 120
Db 85 FIENLLPSDGFWIGLRREKQSNSTACQDLVATDGSISQFRNWXVDEPSCGSEVCV 144

Qy 121 MYHQPAPAGIGGYPFQWDDRCNKNFNICKYSDEKPAVPSREAGEETELTTPVLPE 180
Db 145 MYHQPAPAGIGGYPFQWDDRCNKNFNICKYSDEKPAVPSREAGEETELTTPVLPE 204

Qy 181 ETQEDAKTKFKESREAAALNLAY 203
Db 205 ETQEDAKTKFKESREAAALNLAY 227

RESULT 9
US-10-351-334-166
; Sequence 166, Application US/10351334
; Publication No. US20040034196A1
; GENERAL INFORMATION:
; APPLICANT: Komatsoulis et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P2
; CURRENT APPLICATION NUMBER: US/10/351,334
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/350,898
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/489,847
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: PCT/US99/17130
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/095,486
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/096,319

; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIC, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2142
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-094-749-2142

Query Match          99.6%; Score 1096; DB 15; Length 374;
Best Local Similarity 99.5%; Pred. No. 3.6e-102;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLLSGQVPCRGGTQPCVKIYFHDTSRRLNFEEAKACRRDGGQLVSEDEQKLIK 60
Db 25 RLLSGQVPCRGGTQPCVKIYFHDTSRRLNFEEAKACRRDGGQLVSEDEQKLIK 84

Qy 61 FIENLLPSDGFWIGLRREKQSNSTACQDLVATDGSISQFRNWXVDEPSCGSEVCV 120
Db 85 FIENLLPSDGFWIGLRREKQSNSTACQDLVATDGSISQFRNWXVDEPSCGSEVCV 144

Qy 121 MYHQPAPAGIGGYPFQWDDRCNKNFNICKYSDEKPAVPSREAGEETELTTPVLPE 180
Db 145 MYHQPAPAGIGGYPFQWDDRCNKNFNICKYSDEKPAVPSREAGEETELTTPVLPE 204

Qy 181 ETQEDAKTKFKESREAAALNLAY 203
Db 205 ETQEDAKTKFKESREAAALNLAY 227

RESULT 10
US-09-909-320-137
; Sequence 137, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

```

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-320-137

Query Match 98.7%; Score 1086; DB 9; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLIS-----GQVCRGGTQPCVKVIYFHDTSRLNFEAEAKACRRDGGQLVSIIE 52
Db 25 RLISASDLRLGGQPCVCRGGTQPCVKVIYFHDTSRLNFEAEAKACRRDGGQLVSIIE 84
QY 53 DEQKLEKFIENLLPSDGFWMGLRREERKQSNSTACQDLYAMTDGSIQFRNYYVDEPS 112
Db 85 DEQKLEKFIENLLPSDGFWMGLRREERKQSNSTACQDLYAMTDGSIQFRNYYVDEPS 144
QY 113 CGSEVCVMYHQSAPAGIGPYMFQWQNDRCNMKNFNICKYSDKXPVPSRAEGSETE 172
Db 145 CGSEVCVMYHQSAPAGIGPYMFQWQNDRCNMKNFNICKYSDKXPVPSRAEGSETE 204
QY 173 LTPVLPETQEDAKTKFKESREAAALNLAY 203
Db 205 LTPVLPETQEDAKTKFKESREAAALNLAY 235

RESULT 11
US-09-909-088B-137
; Sequence 137, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-088B-137

Query Match 98.7%; Score 1086; DB 9; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQGVLSIESE 52
    |||||
Db 25 RLLSASDLDLRGQGPVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQGVLSIESE 84
    |||||
QY 53 DEQKLIKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112
    |||||
Db 85 DEQKLIKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 144
    |||||
QY 113 CGSEVVCVMYHQPAPAGIGGYPWFQWDDRCNMKNFICKYDEKPAVPSREAEGETE 172
    |||||
Db 145 CGSEVVCVMYHQPAPAGIGGYPWFQWDDRCNMKNFICKYDEKPAVPSREAEGETE 204
    |||||
QY 173 LTPVLPPEETQEDAKKTFKESREAAALNLAY 203
    |||||
Db 205 LTPVLPPEETQEDAKKTFKESREAAALNLAY 235
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```

RESULT 12

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US-09-905-291A-137
; Sequence 137, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313

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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-137

Query Match 98.7%; Score 1086; DB 9; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQGVLSIESE 52
    |||||
Db 25 RLLSASDLDLRGQGPVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQGVLSIESE 84
    |||||
QY 53 DEQKLIKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112
    |||||
Db 85 DEQKLIKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 144
    |||||
QY 113 CGSEVVCVMYHQPAPAGIGGYPWFQWDDRCNMKNFICKYDEKPAVPSREAEGETE 172
    |||||
Db 145 CGSEVVCVMYHQPAPAGIGGYPWFQWDDRCNMKNFICKYDEKPAVPSREAEGETE 204
    |||||
QY 173 LTPVLPPEETQEDAKKTFKESREAAALNLAY 203
    |||||
Db 205 LTPVLPPEETQEDAKKTFKESREAAALNLAY 235
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RESULT 13

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US-09-902-853-137
; Sequence 137, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313

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FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902.853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-853-130

Query Match 98.7%; Score 1086; DB 9; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
Qy 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQLVSI 52
Db 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQLVSI 84
Qy 53 DEQKLEKFIENLPSDGFWGLRRREKOSNSTACQDLYAWTDGSIQFRWYVDEPS 112
Db 85 DEQKLEKFIENLPSDGFWGLRRREKOSNSTACQDLYAWTDGSIQFRWYVDEPS 144
Qy 113 CGSEVCVMYHQPAPAGIGGPFYFQWDDRCNMKNFIKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCVMYHQPAPAGIGGPFYFQWDDRCNMKNFIKYSDEKPAVPSREAEGETE 204
Qy 173 LTTVPLEETQEDAKKTFKESREAAINLAY 203
Db 205 LTTVPLEETQEDAKKTFKESREAAINLAY 235

RESULT 14
US-09-907-824-137
Sequence 137, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-824-137

Query Match 98.7%; Score 1086; DB 9; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIIE 52
| | | | |
Db 25 RLLSASDLDRGGQVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIIE 84
| | | | |
QY 53 DEQKLIKFIENLPSDGFWMGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112
| | | | |
Db 85 DEQKLIKFIENLPSDGFWMGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 144
| | | | |
QY 113 CGSEVCVVMYHQPAPAGIGPYMFQWDDRCNMKNFICKYSDKPAVPSREAEGETE 172
| | | | |
Db 145 CGSEVCVVMYHQPAPAGIGPYMFQWDDRCNMKNFICKYSDKPAVPSREAEGETE 204
| | | | |
QY 173 LTTPLVPEETOEDAKTFFKESREAAALNAY 203
| | | | |
Db 205 LTTPLVPEETOEDAKTFFKESREAAALNAY 235
| | | | |

RESULT 15

US-09-907-841-137
; Sequence 137, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29

; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-841-137
Query Match 98.7%; Score 1086; DB 9; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIIE 52
| | | | |
Db 25 RLLSASDLDRGGQVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIIE 84
| | | | |
QY 53 DEQKLIKFIENLPSDGFWMGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112
| | | | |
Db 85 DEQKLIKFIENLPSDGFWMGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 144
| | | | |
QY 113 CGSEVCVVMYHQPAPAGIGPYMFQWDDRCNMKNFICKYSDKPAVPSREAEGETE 172
| | | | |
Db 145 CGSEVCVVMYHQPAPAGIGPYMFQWDDRCNMKNFICKYSDKPAVPSREAEGETE 204
| | | | |
QY 173 LTTPLVPEETOEDAKTFFKESREAAALNAY 203
| | | | |
Db 205 LTTPLVPEETOEDAKTFFKESREAAALNAY 235
| | | | |

RESULT 16

US-09-904-011-137
; Sequence 137, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR FILING DATE: 09/665,350
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222

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; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-137

Query Match      98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHTSRLNFEFEAKACRRDGGQLVSIIE 52
Db 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHTSRLNFEFEAKACRRDGGQLVSIIE 84
QY 53 DEQKLIKFIEIENLPSDGFWMGLRRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112
Db 85 DEQKLIKFIEIENLPSDGFWMGLRRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 144
QY 113 CGSEVCVMYHQSPAGIGGPPYFQWDRRCNMKNFICKYSDEKPAVPSRAEGEETE 172
Db 145 CGSEVCVMYHQSPAGIGGPPYFQWDRRCNMKNFICKYSDEKPAVPSRAEGEETE 204
QY 173 LTPVLPPEETQEDAKTKFKESREALNLAY 203
Db 205 LTPVLPPEETQEDAKTKFKESREALNLAY 235

RESULT 17
US-09-906-742-137
; Sequence 137, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-137

Query Match      98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHTSRLNFEFEAKACRRDGGQLVSIIE 52
Db 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHTSRLNFEFEAKACRRDGGQLVSIIE 84
QY 53 DEQKLIKFIEIENLPSDGFWMGLRRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112
Db 85 DEQKLIKFIEIENLPSDGFWMGLRRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 144
QY 113 CGSEVCVMYHQSPAGIGGPPYFQWDRRCNMKNFICKYSDEKPAVPSRAEGEETE 172
Db 145 CGSEVCVMYHQSPAGIGGPPYFQWDRRCNMKNFICKYSDEKPAVPSRAEGEETE 204
QY 173 LTPVLPPEETQEDAKTKFKESREALNLAY 203
Db 205 LTPVLPPEETQEDAKTKFKESREALNLAY 235

```

Db 145 CGSEVVMVTHQPSAPAGIGPYFQWDDRCNNKNNFICKYSDKPAVPSREAGEETE 204

Qy 173 LTTPLPEETQEDAKTKFESREAAALNAY 203
Db 205 LTTPLPEETQEDAKTKFESREAAALNAY 235

RESULT 18

US-09-806-838-137

; Sequence 137, Application US/09906838

; Publication No. US20030027143A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Grimsdall, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/306,838

; CURRENT FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 09/665,350

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 137

; LENGTH: 382

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-09-906-838-137

Query Match 98.7%; Score 1086; DB 10; Length 382;

Best Local Similarity 96.2%; Pred. No. 3.8e-101;

Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

Qy 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEAKACRRDGGQLVSI 52

Db 25 RLLSASDLRLRGQPCVCRGGTQPCYKVIYFHDTSRLNFEAKACRRDGGQLVSI 84

Qy 53 DEOKLIEFIENLLPSDGDGFWIGLRRREEKQSNSTACODLYAWTDGSIQFRNWWYVDEPS 112

Db 85 DEOKLIEFIENLLPSDGDGFWIGLRRREEKQSNSTACODLYAWTDGSIQFRNWWYVDEPS 144

Qy 113 CGSEVVMVTHQPSAPAGIGPYFQWDDRCNNKNNFICKYSDKPAVPSREAGEETE 172

Db 145 CGSEVVMVTHQPSAPAGIGPYFQWDDRCNNKNNFICKYSDKPAVPSREAGEETE 204

Qy 173 LTTPLPEETQEDAKTKFESREAAALNAY 203

Db 205 LTTPLPEETQEDAKTKFESREAAALNAY 235

RESULT 19

US-09-907-613-137

; Sequence 137, Application US/09907613

; Publication No. US20030027145A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Grimsdall, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,613

; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US 09/907,942
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-613-137

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQLVSIIE 52
DB 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQLVSIIE 84
QY 53 DEQKLEKFIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 112
DB 85 DEQKLEKFIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 144
QY 113 CGSEVCVMYHQPSAPAGIGPYMFWQNDRCNKNFICKYSDKPAVPSREAGEETE 172
DB 145 CGSEVCVMYHQPSAPAGIGPYMFWQNDRCNKNFICKYSDKPAVPSREAGEETE 204
QY 173 LTTPLPEETQEBDAKTKFESREAAINLAY 203
DB 205 LTTPLPEETQEBDAKTKFESREAAINLAY 235

RESULT 20
US-09-907-942-137
Sequence 137, Application US/09907942
Publication No. US20030027146A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQLVSIIE 52
DB 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRLNFEAKEACRRDGGQLVSIIE 84
QY 53 DEQKLEKFIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 112
DB 85 DEQKLEKFIENLLPSDGFWIGLRREKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 144

QY 113 CGSEVCVVMYHQSAPAGIGPVMFQWDDRCNNKNNFKICKYSDKPAVPSREAEGETE 172
DB 145 CGSEVCVVMYHQSAPAGIGPVMFQWDDRCNNKNNFKICKYSDKPAVPSREAEGETE 204
QY 173 LTTPLVPEETQEDAKTKFKESREAAALNLAY 203
DB 205 LTTPLVPEETQEDAKTKFKESREAAALNLAY 235
RESULT 21
US-09-904-859-137
; Sequence 137, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-137
Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 RLLS-----GQVCGGTGTCPCYKVIYPHDTSRLNFEAEACRRDGGQLVSI 52
DB 25 RLLSASDLDLGGGQPCVCGGTGTCPCYKVIYPHDTSRLNFEAEACRRDGGQLVSI 84
QY 53 DEQKLIEXFIENLLPDSGDGFWIGLRRREEKQSNSTACQDLYAWTDGSI 112
DB 85 DEQKLIEXFIENLLPDSGDGFWIGLRRREEKQSNSTACQDLYAWTDGSI 144
QY 113 CGSEVCVVMYHQSAPAGIGPVMFQWDDRCNNKNNFKICKYSDKPAVPSREAEGETE 172
DB 145 CGSEVCVVMYHQSAPAGIGPVMFQWDDRCNNKNNFKICKYSDKPAVPSREAEGETE 204
QY 173 LTTPLVPEETQEDAKTKFKESREAAALNLAY 203
DB 205 LTTPLVPEETQEDAKTKFKESREAAALNLAY 235
RESULT 22
US-09-909-204-137
; Sequence 137, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,204
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-204-137

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLIS-----GQVCRGGTQPCYKVIYFHDTSRLNFEBAKEACRRDGGQLVSIIE 52
Db 25 RLISASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRLNFEBAKEACRRDGGQLVSIIE 84
QY 53 DEQKLIKFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112
Db 85 DEQKLIKFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 144
QY 113 CGSEVCVMYHQPSAPAGIGGPMYFQWDDRCNNKNNFICKYSDKPAVPSRAEGEETE 172
Db 145 CGSEVCVMYHQPSAPAGIGGPMYFQWDDRCNNKNNFICKYSDKPAVPSRAEGEETE 204
QY 173 LTTPLPEETQEDAKKTFKESREALNLAY 203
Db 205 LTTPLPEETQEDAKKTFKESREALNLAY 235

RESULT 23
US-09-904-820-137
; Sequence 137, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fliviaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-820-137

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLIS-----GQVCRGGTQPCYKVIYFHDTSRLNFEBAKEACRRDGGQLVSIIE 52
Db 25 RLISASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRLNFEBAKEACRRDGGQLVSIIE 84
QY 53 DEQKLIKFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112

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85 DEQKLEFIENLLPSDGFWDGLRRREKQSNSTACQDLYAMTDGSIQFRNYYVDEPS 144
113 CGSEVCVVMYHQSAPAGIGPYFQWDDRCNNKNNFICKYSDEKPAVPSREAGEETE 172
145 CGSEVCVVMYHQSAPAGIGPYFQWDDRCNNKNNFICKYSDEKPAVPSREAGEETE 204
173 LTTPLVPEETQEDAKKTFKESREAAALNLAY 203
205 LTTPLVPEETQEDAKKTFKESREAAALNLAY 235

RESULT 24
US-09-904-786-137
; Sequence 137, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Klijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,786
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-786-137

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GPFVCGGTQRCYKVIYFHDTSRLNFEAEKACRRGGQLVSTIESE 52
25 RLLSASDLDLRGGQPCVCGGTQRCYKVIYFHDTSRLNFEAEKACRRGGQLVSTIESE 84
QY 53 DEQKLEFIENLLPSDGFWDGLRRREKQSNSTACQDLYAMTDGSIQFRNYYVDEPS 112
85 DEQKLEFIENLLPSDGFWDGLRRREKQSNSTACQDLYAMTDGSIQFRNYYVDEPS 144
QY 113 CGSEVCVVMYHQSAPAGIGPYFQWDDRCNNKNNFICKYSDEKPAVPSREAGEETE 172
145 CGSEVCVVMYHQSAPAGIGPYFQWDDRCNNKNNFICKYSDEKPAVPSREAGEETE 204
QY 173 LTTPLVPEETQEDAKKTFKESREAAALNLAY 203

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DB 205 LTTPLVPEETQEDAKKTFKESREAAALNLAY 235

RESULT 25
US-09-906-646-137
; Sequence 137, Application US/09906646
; Publication No. US20030039971A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Klijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,646
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05

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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-646-137

Query Match      98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

Qy 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEFAKACRRDGGQLVSTSE 52
Db 25 RLLSASDLRLGGQFVCRGGTQPCYKVIYFHDTSRLNFEFAKACRRDGGQLVSTSE 84
Qy 53 DEQKLEKFIENLLPSDGFWGLRRREEKQSNSTACODLYAWTDGSIQFRNMYVDEPS 112
Db 85 DEQKLEKFIENLLPSDGFWGLRRREEKQSNSTACODLYAWTDGSIQFRNMYVDEPS 144
Qy 113 CGSEVCVVMYHQPAPAGIGGYPYMFQWDRCNMKNNFICKYSDKPAVPSREAEGEETE 172
Db 145 CGSEVCVVMYHQPAPAGIGGYPYMFQWDRCNMKNNFICKYSDKPAVPSREAEGEETE 204
Qy 173 LTTPLPEETOEDAKKTFKESREALNLAY 203
Db 205 LTTPLPEETOEDAKKTFKESREALNLAY 235
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Search completed: September 9, 2004, 23:13:11
Job time : 91.2776 secs

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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:50:45 ; Search time 15.9607 Seconds
(without alignments)
656.618 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227

Perfect score: 1100
Sequence: 1 RLLSGQVCRGGTQPCYK.....EEDAKTKFESREALNLAY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1090	99.1	374	4	US-09-489-847-166
2	1086	98.7	382	4	US-09-907-794A-137
3	1086	98.7	382	4	US-09-905-125A-137
4	1086	98.7	382	4	US-09-902-775A-137
5	939.5	85.4	260	4	US-09-638-203-3
6	561.5	51.0	273	4	US-09-638-203-2
7	225	20.5	81	4	US-09-489-847-325
8	225	20.5	82	4	US-09-489-847-234
9	225	20.5	115	4	US-09-489-847-324
10	182	16.5	1456	4	US-09-976-594-168
11	178.5	16.2	1455	3	US-08-840-062-5
12	178.5	16.0	1479	3	US-08-840-062-4
13	174	15.8	1257	1	US-08-340-428B-49
14	174	15.8	2409	6	5180808-2
15	170.5	15.5	1479	3	US-08-840-062-2
16	152	13.8	912	5	PCT-US95-03747-2
17	151	13.7	197	4	US-09-602-877A-99
18	149.5	13.6	455	4	US-09-866-028-50
19	149	13.5	174	1	US-07-641-971B-1
20	149	13.5	174	1	US-07-781-248A-1
21	149	13.5	320	1	US-08-365-103B-10
22	149	13.5	321	1	US-08-365-103B-8
23	148.5	13.5	652	2	US-08-751-305-2
24	144.5	13.1	404	4	US-09-517-605-2
25	143.5	13.0	372	2	US-08-513-278-4
26	143.5	13.0	372	6	5514582-4
27	142	12.9	1487	3	US-08-840-062-7

28	141.5	12.9	125	3	US-08-722-126A-7	Sequence 7, Appl
29	141.5	12.9	125	5	PCT-US95-04258-7	Sequence 7, Appl
30	141.5	12.9	287	1	US-08-365-103B-4	Sequence 4, Appl
31	141.5	12.9	300	1	US-08-365-103B-6	Sequence 6, Appl
32	141.5	12.9	327	1	US-08-365-103B-2	Sequence 2, Appl
33	138.5	12.6	117	6	5514582-7	Patent No. 5514582
34	138.5	12.6	119	1	US-08-340-539A-12	Sequence 12, Appl
35	137.5	12.5	110	6	5514582-12	Patent No. 5514582
36	137.5	12.5	123	6	5514582-19	Patent No. 5514582
37	137.5	12.5	492	4	US-09-724-864-39	Sequence 39, Appl
38	135	12.3	238	3	US-09-111-470-8	Sequence 8, Appl
39	134.5	12.2	128	4	US-09-535-521-8	Sequence 8, Appl
40	134.5	12.2	139	4	US-09-535-521-11	Sequence 11, Appl
41	134.5	12.2	141	4	US-09-535-521-14	Sequence 14, Appl
42	134.5	12.2	167	4	US-09-535-521-17	Sequence 17, Appl
43	134.5	12.2	208	4	US-09-535-521-20	Sequence 20, Appl
44	134.5	12.2	292	4	US-09-535-521-2	Sequence 2, Appl
45	134.5	12.2	292	4	US-09-535-521-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-489-847-166
; Sequence 166, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-166

Query Match 99.1%; Score 1090; DB 4; Length 374;
Best Local Similarity 99.0%; Pred. No. 9.5e-106;
Matches 201; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	RLLSGQVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQGVLSIESEDEQKLIEX	60
DB	25	RLLSGQVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQGVLSIESEDEQKLIEX	84
QY	61	FIENLLPSDGDGFWIGLRREKQKSNSTACQDIYAWTDSISQFRWYVDEPSCGSEVCV	120
DB	85	FIENLLPSDGDGFWIGLRREKQKSNSTXCDLIYAWTDSISQFRWYVDEPSCGSEVCV	144

QY 121 MYHQSAPAGIGPYMFQWDDRCNMKNFICKYSDKPAVPSREAGSETELTTPVLPE 180
 Db 145 MYHQSAPAGIGPYMFQWDDRCNMKNFICKYSDKPAVPSREAGSETELTTPVLPE 204
 QY 181 ETQEDAKTFKESREAAALNLAY 203
 Db 205 ETQEDAKTFKESREAAALNLAY 227

RESULT 2

US-09-907-794A-137
 ; Sequence 137, Application US/09907794A
 ; Patent No. 6635468
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/907,794A
 ; PRIOR FILING DATE: 2001-07-17
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 137
 ; LENGTH: 382
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-907-794A-137
 Query Match 98.7%; Score 1086; DB 4; Length 382;
 Best Local Similarity 96.2%; Pred. No. 2.6e-105;
 Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
 QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQLVSIESE 52
 Db 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQLVSIESE 84
 QY 53 DEQKLEKFIENLPSDGFWIGLRRREKOSNSTACODLYAWTDGSGISQFRNWWVDEPS 112
 Db 85 DEQKLEKFIENLPSDGFWIGLRRREKOSNSTACODLYAWTDGSGISQFRNWWVDEPS 144
 QY 113 CGSEVGVVYHQSAPAGIGPYMFQWDDRCNMKNFICKYSDKPAVPSREAGSETE 172
 Db 145 CGSEVGVVYHQSAPAGIGPYMFQWDDRCNMKNFICKYSDKPAVPSREAGSETE 204
 QY 173 LTPVLPEETQEDAKTFKESREAAALNLAY 203
 Db 205 LTPVLPEETQEDAKTFKESREAAALNLAY 235

RESULT 3

US-09-905-125A-137
 ; Sequence 137, Application US/09905125A
 ; Patent No. 6664376
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/905,125A
 ; PRIOR FILING DATE: 2001-07-12
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698

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; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-137

Query Match 98.7%; Score 1086; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 2.6e-105;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQPVCRGGTQPCYKVIYFHTSRLNFEFEAKACRRDGGQLVSIIE 52
Db 25 RLLSASDLDRGGQPVCRGGTQPCYKVIYFHTSRLNFEFEAKACRRDGGQLVSIIE 84
QY 53 DEQKLIKFIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112
Db 85 DEQKLIKFIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 144
QY 113 CGSEVCVVMYHQPAPAGIGGPFYQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 172
Db 145 CGSEVCVVMYHQPAPAGIGGPFYQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 204
QY 173 LTTPLPEETQEDAKKTFKESREAAALNAY 203
Db 205 LTTPLPEETQEDAKKTFKESREAAALNAY 235

RESULT 4
US-09-902-775A-137
; Sequence 137, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-137

Query Match 98.7%; Score 1086; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 2.6e-105;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQPVCRGGTQPCYKVIYFHTSRLNFEFEAKACRRDGGQLVSIIE 52
Db 25 RLLSASDLDRGGQPVCRGGTQPCYKVIYFHTSRLNFEFEAKACRRDGGQLVSIIE 84
QY 53 DEQKLIKFIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 112
Db 85 DEQKLIKFIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEPS 144
QY 113 CGSEVCVVMYHQPAPAGIGGPFYQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 172
Db 145 CGSEVCVVMYHQPAPAGIGGPFYQWDDRCNMKNFICKYSDEKPAVPSREAGEETE 204
QY 173 LTTPLPEETQEDAKKTFKESREAAALNAY 203
Db 205 LTTPLPEETQEDAKKTFKESREAAALNAY 235
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Db 145 CGSEVGVVYHQPAPAGIGPYFMQWDDRCNMKNFICKYSDKFAVPSREAGEETE 204
QY 173 LTTVPVLEETQEDAKTKFKESREAAALNAY 203
Db 205 LTTVPVLEETQEDAKTKFKESREAAALNAY 235

RESULT 5
US-09-638-203-3
; Sequence 3, Application US/09638203
; Patent No. 6602501
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Ava Jakobovits
; APPLICANT: Arthur B. Raitano
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF
; FILE REFERENCE: 129.20USU1
; CURRENT APPLICATION NUMBER: US/09/638,203
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,935
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Hamster
US-09-638-203-3

Query Match 85.4%; Score 939.5; DB 4; Length 260;
Best Local Similarity 85.8%; Pred. No. 3.2e-90;
Matches 175; Conservative 9; Mismatches 19; Indels 1; Gaps 1;

QY 1 RLLSQPVCRGQGTQPCYKVIYFHDTSRRLNFEAKACRRDGGQLVSISEDEQKLEK 60
Db 1 RLLSQVLVCRGTRPCYKVIYFHDQRLNFEAKACRRDGGQLVSIETEDQRLIEK 60
QY 61 FIENLLPSDGFWTGLRRREKQSNSTACQDLYAWTDGSIQFRNMYVDPSPCGSEVCVV 120
Db 61 FIENLLASDGFWTGLRRLEVKQVNTACQDLYAWTDGSIQFRNMYVDPSPCGSEVCVV 120
QY 121 MYHQPAPAGIGPYFMQWDDRCNMKNFICKYSDKFAVPSREAGEETELTTPVLP 179
Db 121 MYHQPAPPGIGGYSYFMQWDDRCNMKNFICKYADEKPTTPIRPGGATEPTTPVLP 180
QY 180 EETQEDAKTKFKESREAAALNAY 203
Db 181 EETQEDAKTKFKESREAAALNAY 204

RESULT 6
US-09-638-203-2
; Sequence 2, Application US/09638203
; Patent No. 6602501
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Ava Jakobovits
; APPLICANT: Arthur B. Raitano
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF
; FILE REFERENCE: 129.20USU1
; CURRENT APPLICATION NUMBER: US/09/638,203
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,935
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 273
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-638-203-2

Query Match 51.0%; Score 561.5; DB 4; Length 273;
Best Local Similarity 60.1%; Pred. No. 1.2e-50;
Matches 101; Conservative 25; Mismatches 35; Indels 7; Gaps 3;

QY 1 RLLSQPVCRGQGTQPCYKVIYFHDTSRRLNFEAKACRRDGGQLVSISEDEQKLEK 60
Db 23 RVVSQKVCFADFKHPCYKMAFYHELSRSVFSQEARLACESEGGVLLSLENAEQKLI 82
QY 61 FIENLLP-----SQDFFWGLRRREKQSNSTACQDLYAWTDGSIQFRNMYVDPSPCGS 115
Db 83 MLQNLTKFTGISDGFWTGLWRNGDGT-SGACPDLYQWSDGSGNSQYRNWYTDPSGCS 141
QY 116 EVCVVMYHQPAPAGIGPYFMQWDDRCNMKNFICKYSDKFAVPS 162
Db 142 EKCVMYHQPAPAGIGPYFMQWDDRCNMKNFICKYSDKFAVPS 189

RESULT 7
US-09-489-847-325
; Sequence 325, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 325
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-325

Query Match 20.5%; Score 225; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.6e-16;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSQPVCRGQGTQPCYKVIYFHDTSRRLNFEAKACRR 41
Db 25 RLLSQPVCRGQGTQPCYKVIYFHDTSRRLNFEAKACRR 65

RESULT 8
US-09-489-847-234
; Sequence 234, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
```

```
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 234
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (82)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-234

Query Match          20.5%; Score 225; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 3.6e-16;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLSGQVCRGGTQPCVKVIYFHTSRLNFEAKEACRR 41
Db 25 RLLSGQVCRGGTQPCVKVIYFHTSRLNFEAKEACRR 65

RESULT 9
US-09-489-847-324
; Sequence 324, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 324
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-324

Query Match          20.5%; Score 225; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.7e-16;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLSGQVCRGGTQPCVKVIYFHTSRLNFEAKEACRR 41
Db 59 RLLSGQVCRGGTQPCVKVIYFHTSRLNFEAKEACRR 99

RESULT 10
US-09-976-594-168
; Sequence 168, Application US/09976594
; Patent No. 6673549
```

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; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 168
; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1674368CD1
US-09-976-594-168

Query Match          16.5%; Score 182; DB 4; Length 1456;
Best Local Similarity 25.5%; Pred. No. 5.6e-10;
Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;

Qy 18 YKVIYFHTSRLNFEAKEACRRDGGQGVSTSEDEOKLIEKFIENLLPSDGDWIGLR 77
Db 807 YKDYQYFSEKETWDMNAPFCRNFGLVSIQSEKFLWKYV-NRNDASAYFIGLL 865
Qy 78 RREXQSNSTACQDLYANTDGSISQFRNMYVDEPSCGS--EVCVVMYHQPSPAPAGIGOPY 135
Db 866 ISLDKK-----FAWMDGSKVDYVSWATGEPNANEDENCVTWY----SNSGF---- 908
Qy 136 MFQWDDRCNMKNRICKYSDK-----PAVPSREAGSETELTTPVLPEETOE----- 184
Db 909 ---WNDINGYFNATICQHNSSINATTVMP-----TMPSPVSGCKEGWNFYSN 954
Qy 185 -----EDAKTFKESREAAAL 199
Db 955 KCFKIFGFMEERKNWQEARKACI 978

RESULT 11
US-08-840-062-5
; Sequence 5, Application US/08840062
; Patent No. 6117977
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: WU, KAI
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,062
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1019R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
```

TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-840-062-5

Query Match 16.2%; Score 178.5; DB 3; Length 1455;
Best Local Similarity 25.9%; Pred. No. 1.3e-09;
Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;

QY 18 YKVIYFHTSRRLNFEAKACRRDGGQLVSISEDEQKLEKFIENLLPSDGFVIGLR 77
DB 806 YKDYQYVFSKETMDNARRFKCNFGDLATIKSESKFLWKYI-NKNGGQSPYFIGML 864
QY 78 RREEKQNSTACQDLYAWTSGISQFRNYYVDEPSCGS--EVCVVMYHQPAPAGIGGPY 135
DB 865 ISMDKK-----FIWMDGSKVDVAMATGEBFNFDNDNCVTWY---TNSGF--- 907
QY 136 MFQWDDRCNNKNPFICK---YSDEKPAVPSREAGEETELTPVLPEETQE----- 184
DB 908 ---WNDINCGYPNNFICORHNSSINATAMP-----TTPTPGCKGEGHLYKNK 953
QY 185 -----EDAKTKFESREALNL 201
DB 954 CFKIFGANEEKSKWQARQCKGL 978

RESULT 12
US-08-840-062-4
Sequence 4, Application US/08840062
Patent No. 6117977
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: WU, KAI
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: US/08/840.062
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1019R1
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1479 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-840-062-4

Query Match 16.0%; Score 176.5; DB 3; Length 1479;
Best Local Similarity 30.4%; Pred. No. 2.2e-09;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;

QY 4 SGQVRCGTQPCYKVIYFHTSRRLNFEAKACRRDGGQLVSISEDEQKLEKFIEN 63
DB 385 SWQPP-----QHCYRL-----QAEKSWQSKACLRGGDLVSIHMAELEFITQIK 434
QY 64 NLLPSDGFVIGLRREEKQNSTACQDLYAWTSGISQFRNYYVDEPSCGS---CGSEVCVV 120
DB 435 QEVE---ELWIGL-----NDLKLQWNFWSGSLVSEFTHMHPFPNFRDLSLDCVT 483
QY 121 MYHQPAPAGIGGPYMFQWDDRCNNKNPFICKYSDEKPAVPSREAGS 168
DB 484 IW---GPEG-----RWNDSPCNQSLPSICKKAGQLSQGAASEDHG 520

RESULT 13
US-08-340-428B-49
Sequence 49, Application US/08340428B
Patent No. 5648465
GENERAL INFORMATION:
APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: MARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340.428B
FILING DATE: 14 No. 5648465ember 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922.911
FILING DATE: 03 August 1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Margolis=1A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-340-428B-49

Query Match 15.8%; Score 174; DB 1; Length 1257;
Best Local Similarity 30.8%; Pred. No. 3.2e-09;
Matches 44; Conservative 18; Mismatches 49; Indels 32; Gaps 6;

QY 14 QPCYKVIYFHTSRRLNFEAKACRRDGGQLVSISEDEQKLEKFIENLLPSDGFV 73
DB 1037 QGHCYR--YF---AHRRAWEDAERDCRRRAGHLTVHSPFHEKFINSP-----CHENSW 1085
QY 74 IGLRREEKQNSTACQDLYAWTSGISQFRNYYVDEPSCGS---CGSEVCVVMYHQPAPAG 130
DB 1086 IGLNDETVERD-----FQWTDNTGLQYENWREKQPDNPFAGGDCVVMVAHENG--- 1134
QY 131 IGGPYNFQWDDRCNNKNPFICK 153

RESULT 17
 US-09-602-877A-99
 ; Sequence 99, Application US/09602877A
 ; Patent No. 6432707
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, David C.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.446C5
 ; CURRENT APPLICATION NUMBER: US/09/602.877A
 ; CURRENT FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 99
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-602-877A-99

Query Match 13.7%; Score 151; DB 4; Length 197;
 Best Local Similarity 25.0%; Pred. No. 6.5e-08;
 Matches 38; Conservative 26; Mismatches 54; Indels 24; Gaps 4;
 QY 6 QPVRGGTQ--RPGYKVIYFHTSRLNFEBAKACRRDGGQLVSISEDEQKLIKPIE 63
 DB 65 QTVCLRGTKVHKCYLA-----SEGLKHFHEANEDCISKGILVIPRNSDEINALQDYGK 119
 QY 64 NLLPSDGFVWGLARRREKQNSACODLYAWTDGSIQFNWTVDPSCGSEVGVVMYH 123
 DB 120 RSLFGVDFWLG-----NDVATGKFDVYNGIAISFLNWDRAQPNKGKRENCVLFS 171
 QY 124 QPSAPAGIGPYFMQWDDRCNMKNFKICKYS 155
 DB 172 QSA-----QGWSDACRSKRYICEPT 194

RESULT 18
 US-09-866-028-50
 ; Sequence 50, Application US/09866028
 ; Patent No. 6642360
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kljavin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tamas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT APPLICATION NUMBER: US/09/866.028
 ; CURRENT FILING DATE: 2001-05-25
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 50
 ; LENGTH: 455
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-866-028-50

Query Match 13.6%; Score 149.5; DB 4; Length 455;
 Best Local Similarity 25.6%; Pred. No. 2.9e-07;
 Matches 45; Conservative 25; Mismatches 61; Indels 45; Gaps 8;
 QY 11 GGTORPCYKVIY--FHTSRLN-----FEEAKEACRRDGGQLVSISEDEQK 56
 DB 287 GGAQ--CATKVHFPHTCDLRIDGCFVVSSEADTYIYARMKCKQKGVLAQIKSQKVQD 344
 QY 57 LIEKFIENLLP---SDGD-----FWIGLRRREKQNSACODLYAWTDGSIQFNWY 107
 DB 345 ILAFYLGRLTNEVTDSDFETRFNFWIGLTYKTAK-----DSFRWATGEHQAFISFA 396
 QY 108 VDPSGCGSEVGVVMYHQBAPAGIG-----GPFYFMQWDDRCNMKNFKICKYSDE 157
 DB 397 FGQPDNHLGLVWL-----SAAMGFNCVLEQLASAFNWNDRCKTRNYICQPAQE 446

RESULT 19
 US-07-641-971B-1
 ; Sequence 1, Application US/07641971B
 ; Patent No. 5236706
 ; GENERAL INFORMATION:
 ; APPLICANT: Debre, Patrice
 ; APPLICANT: Mossalayi, Mohammed D
 ; TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE
 ; TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation
 ; STREET: 556 Morris Avenue
 ; CITY: Summit
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07901
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/641.971B
 ; FILING DATE: 19910116
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 90016254
 ; FILING DATE: 24-JAN-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fishman, Irving M
 ; REGISTRATION NUMBER: 30258
 ; REFERENCE/DOCKET NUMBER: 4-17921/+/DEB
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 908-277-4832
 ; TELEFAX: 908-277-4306
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 174 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; CELL TYPE: Human B. Cells
 ; CELL LINE: CHO cells transformed with pCAL8-BF-ND
 US-07-641-971B-1

Query Match 13.5%; Score 149; DB 1; Length 174;
 Best Local Similarity 30.2%; Pred. No. 8.9e-08;
 Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;
 QY 14 QRPCYKVIYFHTSRLNFEBAKACRRDGGQLVSISEDEQKLIKPIEENLLPSDGFV 73

Db 24 QKCY---YFGKGTQ--WHARYACDDMEGLVSIHSPEDQLTKH-----ASHTGSW 73
QY 74 IGLRREKQSNSTACQDLYAWTDGSIQFRNMYVDEPSCGS--EVCVMYHQPAPAGI 131
Db 74 IGLNLDLKG-----FIWVDSHVDYSNAPGPTSRSGEDCVMM-----RGS 118
QY 132 GGPYFQWDDRCNMK--NNFICKYSDKPAV---PSREAGE-----ETELTPV 177
Db 119 G-----RWDAFCDRKLGAWC-----DRLATCTPPASEGSAESMGPDSPDPGRUPTPS 169
QY 178 LP 179
Db 170 AP 171

RESULT 20
US-07-781-248A-1
; Sequence 1, Application US/07781248A
; Patent No. 5246699
; GENERAL INFORMATION:
; APPLICANT: Debre, Patrice
; APPLICANT: Mosealayi, Mohammed D
; TITLE OF INVENTION: MATURATION OF HEMATOPOIETIC CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation
; STREET: 556 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07781.248A
; FILING DATE: 19911230
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 90103565
; FILING DATE: 09-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ikeler, Barbara J.
; REGISTRATION NUMBER: 36,170
; REFERENCE/DOCKET NUMBER: 4-18065/A/DEB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-277-3368
; TELEFAX: 908-277-4306
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; CELL TYPE: Human B. Cells
; CELL LINE: CHO cells transformed with pCAL8-BF-ND
US-07-781-248A-1

Query Match 13.5%; Score 149; DB 1; Length 174;
Best Local Similarity 30.2%; Pred. No. 8.9e-08;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;
QY 14 QRPCKVIYFHDTSRLNFEAKEACRDDGGLVSIHSPEDQLTKH-----ETELTPV 73
Db 24 QKCY---YFGKGTQ--WHARYACDDMEGLVSIHSPEDQLTKH-----ASHTGSW 73

QY 74 IGLRREKQSNSTACQDLYAWTDGSIQFRNMYVDEPSCGS--EVCVMYHQPAPAGI 131
Db 74 IGLNLDLKG-----FIWVDSHVDYSNAPGPTSRSGEDCVMM-----RGS 118
QY 132 GGPYFQWDDRCNMK--NNFICKYSDKPAV---PSREAGE-----ETELTPV 177
Db 119 G-----RWDAFCDRKLGAWC-----DRLATCTPPASEGSAESMGPDSPDPGRUPTPS 169
QY 178 LP 179
Db 170 AP 171

RESULT 21
US-08-365-103B-10
; Sequence 10, Application US/08365103B
; Patent No. 5766943
; GENERAL INFORMATION:
; APPLICANT: Lynch, Richard G
; APPLICANT: Nunez, Raphael D.
; APPLICANT: Yodoi, Jungi
; TITLE OF INVENTION: DNA Sequences for Soluble Proms of CD23
; TITLE OF INVENTION: and Methods of Use for Same
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
; STREET: 801 Grand Ave. Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365.103B
; FILING DATE: 28-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nebel, Heidi S.
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: Uif N5-24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 288-3667
; TELEFAX: (515) 288-1338
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-365-103B-10

Query Match 13.5%; Score 149; DB 1; Length 320;
Best Local Similarity 30.2%; Pred. No. 2e-07;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;
QY 14 QRPCKVIYFHDTSRLNFEAKEACRDDGGLVSIHSPEDQLTKH-----ASHTGSW 73
Db 170 QKCY---YFGKGTQ--WHARYACDDMEGLVSIHSPEDQLTKH-----ASHTGSW 219
QY 74 IGLRREKQSNSTACQDLYAWTDGSIQFRNMYVDEPSCGS--EVCVMYHQPAPAGI 131
Db 220 IGLNLDLKG-----FIWVDSHVDYSNAPGPTSRSGEDCVMM-----RGS 264
QY 132 GGPYFQWDDRCNMK--NNFICKYSDKPAV---PSREAGE-----ETELTPV 177
Db 265 G-----RWDAFCDRKLGAWC-----DRLATCTPPASEGSAESMGPDSPDPGRUPTPS 315
QY 178 LP 179

Db 316 AP 317

US-08-365-103B-8

RESULT 22

Sequence 8, Application US/08365103B

Patent No. 5766943

GENERAL INFORMATION:

APPLICANT: Lynch, Richard G

APPLICANT: Nunez, Raphael D.

APPLICANT: Yodoi, Junji

TITLE OF INVENTION: DNA Sequences for Soluble Forms of CD23

TITLE OF INVENTION: and Methods of Use for Same

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Zarley, McKee, Thomte, Voorhees & Sease

STREET: 801 Grand Ave. Suite 3200

CITY: Des Moines

STATE: Iowa

COUNTRY: United States

ZIP: 50309

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/365,103B

FILING DATE: 28-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Nebel, Heidi S.

REGISTRATION NUMBER: 37,719

REFERENCE/DOCKET NUMBER: Uirf N5-24

TELECOMMUNICATION INFORMATION:

TELEPHONE: (515) 288-3667

TELEFAX: (515) 288-1338

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 321 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-365-103B-8

Query Match 13.5%; Score 149; DB 1; Length 321;

Best Local Similarity 30.2%; Pred. No. 2e-07; Indels 50; Gaps 11;

Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY 14 QRCYKVIYFHTSRRLNFEAKACRRDGGQLVSIKIEFKFIENLPLSDGDFW 73

Db 171 QRCYKVIYFHTSRRLNFEAKACRRDGGQLVSIKIEFKFIENLPLSDGDFW 73

QY 74 IGLRRREKQSNSTACQDLVYWTGSIQFRNWTVDPSGCS--EVCVWYHPSAPAGI 131

Db 221 IGLRNLKGE-----FIWVDSGHVDSYNWAPGFTSRSGQEDCVW-----RGS 265

QY 132 GGPYMFQWDDRCNMK--NPFCKYSDEKPAV---PSREAGE-----ETELTTPV 177

Db 266 G-----RWDAFCRKLGAWC-----DLATCTPPASEGSAESMGPSRDPDPGRUPTPS 316

QY 178 LP 179

Db 317 AP 318

RESULT 23

US-08-751-305-2

Sequence 2, Application US/08751305

Patent No. 5965439

GENERAL INFORMATION:

APPLICANT: Tenner et al., Andrea J.

TITLE OF INVENTION: HOST DEFENSE ENHANCEMENT

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/751,305

FILING DATE: 18-NOV-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Wetherell, Jr., John R.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: 07306/012001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 652 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-751-305-2

Query Match 13.5%; Score 148.5; DB 2; Length 652;

Best Local Similarity 24.4%; Pred. No. 6e-07; Indels 43; Gaps 9;

Matches 50; Conservative 37; Mismatches 75; Indels 43; Gaps 9;

QY 2 LLSGQP-----VCRGTCRCPYKVIYFHTSRRLNFEAKACRRDGGQLVSIKIE 50

Db 13 LLLTOPGAGTGADTEAVVVG---TACYTA-----HSGKLSAAEAQNHCNONGNLATVK 64

QY 51 SEDEOKLIEKFIENLPLSD-----GDFWGLRRREKQSNSTACQDLVYWT-DGSISQ 102

Db 65 SXEEAQHVQRLAQLLREAAALTARMSKFWIGLQREKGLCLDPLKGFWSWGGEDTP 124

QY 103 FENWYVD-EPSCGSEVCVW---YHPSAPAGIGGPFYFQWDDRCNMKN-----FI 151

Db 125 YSNWKELRNSCISKRCVSLILLDLSQPLLPNLP-----KWSGPGSGSPGSGNIEGFV 179

QY 152 KYSDEKPAVPSREAGEETELTTP 176

Db 180 CKFSKGMCRPLALGGPGQVTVTTP 204

RESULT 24

US-09-517-605-2

Sequence 2, Application US/09517605

Patent No. 6391567

GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

APPLICANT: Kwon, Douglas S.

APPLICANT: van Kooyk, Yvette

APPLICANT: Geijtenbeek, Theo

TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO

TITLE OF INVENTION: CELLS

FILE REFERENCE: 1049-1-017

CURRENT APPLICATION NUMBER: US/09/517,605

CURRENT FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 404

TYPE: PRT

ORGANISM: Homo sapiens

US-09-517-605-2

Query Match 13.1%; Score 144.5; DB 4; Length 404;
Best Local Similarity 29.7%; Pred. No. 8.3e-07;
Matches 47; Conservative 23; Mismatches 47; Indels 41; Gaps 10;
Qy 22 YHDTSRRLNFEAKEACRDGGOLYSIESDEQKLIETIENLLP-SDGDFWIGLRRREE 81
Db 268 YFMSNSQR-NWHDGSIATCKEVAQLVVKSAEQNFLOQSSR---SNRFTWGLSLNQ 323
Qy 82 KQSNSTACQDLYAWTDS--ISQFEN-WYVDEP-SCGSEVCVMYHQPAPAGIGPYMF 137
Db 324 -----EGTWQVGDSPULPSPKQYNRGEFNNVGEEDCABF-----SNGN----- 363
Qy 138 QWNDRCNMKNFKICKYS-----DEK-----PAVPS 163
Db 364 -WDDKCNLAKFWICKXSAARCSDEDEQFLSPAPATEN 400

RESULT 25

US-08-513-278-4
; Sequence 4, Application US/08513278
; Patent No. 5840844
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: STACHELL, SCOTT E.
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: SINGER, MARK S.
; APPLICANT: YEDNOCK, TED A.
; TITLE OF INVENTION: LYMPHOCTE HOMING RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,278
; FILING DATE: 10-AUG-1995
; CLASSIFICATION: 5530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059027
; FILING DATE: 06-MAY-1993
; APPLICATION NUMBER: 07/786149
; FILING DATE: 31-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 565D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-513-278-4

Query Match 13.0%; Score 143.5; DB 2; Length 372;
Best Local Similarity 26.5%; Pred. No. 9.4e-07;
Matches 41; Conservative 37; Mismatches 50; Indels 27; Gaps 8;

Qy 23 FHDTSRRLNFEAKEACRDGGOLYSIESDEQKLIETIENLLP-SDGDFWIGLRRREE 81
Db 41 YHSEKPMWENARKFCCKONYTDLVAIQNRB---IE-YLENTLPKSPYYWIGIRK--- 93
Qy 82 KQSNSTACQDLYAW--TDGSIS-QFRNMYVDEPS--CGSEVCVMYHQPAPAGIGPYM 136
Db 94 -----IGKMWTVGTNKTLTKEAENWAGGEPNNKSKEDCCEIYIKRERDSG----- 140
Qy 137 FQWDDRCNMKNFKICKYSDEKPAVPSREAEGET 171
Db 141 -KWDDACHKRAALCYTASQPGSCNGRGECEVET 174

Search completed: September 9, 2004, 22:58:16
Job time : 16.9507 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:39:44 ; Search time 85,7101 Seconds
(without alignments)
672.496 Million cell updates/sec

Title: US-09-887-855-2_COPY_24_227

Perfect score: 1106

Sequence: 1 GRLLSGQPVCRGGTQRCPYK.....EEDAKTKFKESREALNLAY 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1106	100.0	374	3 AAY93948	Aay93948 Amino aci
2	1106	100.0	374	4 ABO03651	Aae03651 Human ext
3	1106	100.0	374	5 ABB90203	Abb90203 Human pol
4	1106	100.0	374	6 ABG66680	Abg66680 Human nov
5	1106	100.0	374	6 ADA54522	Ada54522 Human pro
6	1106	100.0	387	4 AAM25796	Aam25796 Human pro
7	1102	99.6	374	6 ADA54574	Ada54574 Human pro
8	1096	99.1	374	3 AAY91490	Aay91490 Human sec
9	1092	98.7	382	2 AAY13367	Aay13367 Amino aci
10	1092	98.7	382	3 ADC78457	Adc78457 Human PRO
11	1092	98.7	382	4 AAB80235	Aab80235 Human PRO
12	1092	98.7	382	4 AAU29033	Aau29033 Human PRO
13	1092	98.7	382	6 ABUS8409	Abu58409 Human PRO
14	1092	98.7	382	6 ABU71613	Abu71613 Human PRO
15	1092	98.7	382	6 ABU87957	Abu87957 Novel hum
16	1092	98.7	382	6 ABU84272	Abu84272 Human sec
17	1092	98.7	382	6 ABR66146	Abr66146 Human sec
18	1092	98.7	382	6 ABR65536	Abr65536 Human sec
19	1092	98.7	382	6 ABUS9476	Abu99476 Human sec
20	1092	98.7	382	6 ABUS2715	Abu82715 Human PRO
21	1092	98.7	382	6 ABUS9836	Abu98936 Novel hum
22	1092	98.7	382	6 ABU71488	Abu71488 Human PRO
23	1092	98.7	382	6 ABR68085	Abr68085 Human sec
24	1092	98.7	382	6 ABUS96138	Abu96138 Novel hum
25	1092	98.7	382	6 ABUS2569	Abu92569 Human sec

ALIGNMENTS

RESULT 1

AAY93948

ID AAY93948 standard; protein; 374 AA.

XX AC AAY93948;

XX DT 03-OCT-2000 (first entry)

XX DE Amino acid sequence of a lectin ss3939 polypeptide.

XX KW Human; lectin ss3939; chromosome 11; gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..21 "signal peptide"

FT Domain 22..227

FT Domain /note= "extracellular coding region"

FT Domain 228..248

FT Domain /note= "predicted transmembrane domain"

FT Domain 249..374

FT Domain /note= "predicted cytoplasmic or intracellular domain"

XX WO200039296-A1.

XX PD 06-JUL-2000.

XX PF 22-DEC-1999; 99WO-US030523.

XX PR 23-DEC-1999; 98US-0113820P.

XX PA (IMMV) IMMUNEX CORP.

XX PI Anderson DA;

XX DR WPI: 2000-452394/39.

XX DR N-PSDB; AAA57382.

PT ss3939 nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it.

XX Claim 12; Page 8; 73pp; English.

XX CC The present sequence represents a human lectin ss3939 polypeptide. The polynucleotide sequence is a source of probes, which may be used to identify nucleic acids encoding ss3939 proteins, to identify human chromosome number 11, to map genes on human chromosome number 11, to

XX CC identify nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it.

CC identify diseases associated with chromosome 11, as single-stranded sense
CC or antisense oligonucleotides to inhibit expression of polypeptides
CC encoded by the ss3939 gene, and for gene therapy. The ss3939 polypeptides
CC may be useful for developing treatments for diseases (none specified).
CC associated with defective or insufficient amounts of the polypeptides.
CC The antibodies may be useful for detecting the presence of ss3939
CC polypeptides
XX
XX
XX Sequence 374 AA;

Query Match 100.0%; Score 1106; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRLLSGQPVCRGQTPCYKVIYFHDTSRLNFEAEACRRDGGQGLVSISSDEQKLE 60
Db 24 GRLLSGQPVCRGQTPCYKVIYFHDTSRLNFEAEACRRDGGQGLVSISSDEQKLE 83
Qy 61 KFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNMYWDEPSCGSEVCV 120
Db 84 KFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNMYWDEPSCGSEVCV 143
Qy 121 VMYHQPAPAGIGGPPYFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTTPVLP 180
Db 144 VMYHQPAPAGIGGPPYFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTTPVLP 203
Qy 181 EETQEDAKKTFKESREAAINLAY 204
Db 204 EETQEDAKKTFKESREAAINLAY 227

RESULT 2
AAE03651
ID AAE03651 standard; protein; 374 AA.

AC AAE03651;
XX
XX 06-AUG-2001 (first entry)
XX Human extracellular matrix and cell adhesion molecule-15 (XMAD-15).
DE
DE Human; extracellular matrix and cell adhesion molecule; XMAD;
KW Gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia;
KW Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy;
KW sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
KW inflammatory disorder; acquired immune deficiency syndrome; AIDS;
KW Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma;
KW Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer;
KW glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis;
KW osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis;
KW infection; cell proliferative disorder; actinic keratosis; myeloma;
KW arteriosclerosis; neutropenic; anticonvulsant; antithyroid; nephrotropic;
KW neuroprotective; dermatological.
XX
XX Homo sapiens.

Key Location/Qualifiers
FT 1..24 /label= Signal_peptide
FT 25..374 /note= "Mature human extracellular matrix and cell adhesion molecule (XMAD)"
FT /note= "C-type lectin domain"
FT 46..63 /note= "C-type lectin domain"
FT 163..176 /note= "C-type lectin domain"
FT 224..247 /note= "Transmembrane motif"
FT 328..348 /note= "Transmembrane motif"
XX
XX WO200142285-A2.

PD 14-JUN-2001.
XX
XX 05-DEC-2000; 2000WO-US032990.
XX
XX 10-DEC-1999; 99US-0172852P.
XX 16-DEC-1999; 99US-0172354P.
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H, Tang YT, Lal P, Burford N, Azimzai Y, Patterson C;
PI Baughn MR, Lu DAM, Shah P, Au-Young J;
PI
DR WPI; 2001-381632/40.
DR N-PSDB; AAD08059.
XX
XX New human extracellular matrix and cell adhesion molecules and
PT polynucleotide sequences encoding them, useful for diagnosis, prevention,
PT treatment of genetic, autoimmune and cell proliferative disorders.
XX
XX Claim 1; Page 108-109; 135pp; English.

XX The present sequence is a human extracellular matrix and cell adhesion
XX molecule (XMAD). The XMAD is used for screening a compound for
XX effectiveness as an agonist or antagonist of XMAD. The identified agonist
XX or antagonist are used for treating a disease or condition associated
XX with decreased or increased expression of functional XMAD. The
XX polynucleotides encoding XMAD are useful in somatic or germline gene
XX therapy to correct a genetic deficiency, to express a conditionally
XX lethal gene product and to express a protein which affords protection
XX against intracellular parasites and also for diagnosis of disorders
XX associated with expression of XMAD. They are also used for generating
XX hybridisation probes useful in mapping the naturally occurring genomic
XX sequences and to create knock in humanised animals (pigs) or transgenic
XX animals (mice or rats) to model human diseases. Oligonucleotide or longer
XX fragments derived from the polynucleotide sequences may be used as
XX elements on a microarray. Antibodies which specifically bind XMAD may be
XX used for the diagnosis of disorders associated with the expression of
XX XMAD, or in assays to monitor patients being treated with XMAD. Diseases
XX diagnosed, prevented or treated include genetic disorders such as
XX adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's
XX disease, myotonic dystrophy, sickle cell anaemia, thalassaemia,
XX autoimmune/inflammatory disorders such as acquired immune deficiency
XX syndrome (AIDS), Addison's disease, allergies, anaemia, asthma,
XX atherosclerosis, Crohn's disease, diabetes mellitus, atopic dermatitis,
XX glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthritis,
XX osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis,
XX bacterial, fungal, parasitic, protozoal and helminthic infections and
XX cell proliferative disorders such as actinic keratosis, arteriosclerosis
XX and cancer including breast, bladder, bone marrow, brain and uterus
XX cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma
XX
XX Sequence 374 AA;

Query Match 100.0%; Score 1106; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GRLLSGQPVCRGQTPCYKVIYFHDTSRLNFEAEACRRDGGQGLVSISSDEQKLE 60
Db 24 GRLLSGQPVCRGQTPCYKVIYFHDTSRLNFEAEACRRDGGQGLVSISSDEQKLE 83
Qy 61 KFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNMYWDEPSCGSEVCV 120
Db 84 KFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNMYWDEPSCGSEVCV 143
Qy 121 VMYHQPAPAGIGGPPYFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTTPVLP 180
Db 144 VMYHQPAPAGIGGPPYFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTTPVLP 203
Qy 181 EETQEDAKKTFKESREAAINLAY 204
Db 204 EETQEDAKKTFKESREAAINLAY 227

RESULT 3
ABE90203
ID ABB90203 standard; protein; 374 AA.
XX
AC ABB90203;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2579.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
FN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016450.
XX
PR 19-MAY-2000; 2000US-0205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
XX
DR N-PSDB; ABL90612.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive, and
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
XX
PS Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 374 AA;
Query Match 100.0%; Score 1106; DB 5; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRLLSGQVCGGTQRCYKVIYFHDTSRLNFEAKACRRDGGQGVLSIESDEQKLI 60
DB 24 GRLLSGQVCGGTQRCYKVIYFHDTSRLNFEAKACRRDGGQGVLSIESDEQKLI 83
QY 61 KFIENLLPSGDGFWIGLRREERQSNSTACQDIYAWTDGSIQFRWYVDEPSCGSEVCV 120
DB 84 KFIENLLPSGDGFWIGLRREERQSNSTACQDIYAWTDGSIQFRWYVDEPSCGSEVCV 143

QY 121 VMYHQSAPAGIGGPNFQWDDRCNKNFNICKYSDEKPAVPSREAGEETELTTPVLP 180
DB 144 VMYHQSAPAGIGGPNFQWDDRCNKNFNICKYSDEKPAVPSREAGEETELTTPVLP 203
QY 181 EETQEEEDAKKTPKESREAAALNLAY 204
DB 204 EETQEEEDAKKTPKESREAAALNLAY 227

RESULT 4
ABG66680
ID ABG66680 standard; protein; 374 AA.
XX
AC ABG66680;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human novel polypeptide #15.
XX
KW Human; inflammatory condition; shock; sepsis; immune response; cancer;
KW wound healing; central nervous system disease; haematopoiesis;
KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
KW bone degenerative disorder; periodontal disease; reperfusion injury;
KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
KW allergic condition; thrombolysis; thrombosis; coagulation disorder;
KW fungal infection.
XX
OS Homo sapiens.
XX
FN WO200244340-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US047004.
XX
PR 30-NOV-2000; 2000US-00728952.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D,
PI Yamazaki V, Ujwal ML, Drmanac RT;
XX
DR WPI; 2002-508509/54.
XX
DR N-PSDB; ABK94904.
XX
PT Novel nucleic acids and polypeptides for diagnosis, treatment of
PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
PT disorders, cancer and promoting wound healing.
XX
PS Claim 10; Page 579-580; 672pp; English.
XX
CC The invention relates to human novel polynucleotides and associated
CC polypeptides. The polynucleotides and polypeptides are useful for
CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
CC and cancer and for promoting wound healing. The sequences are used to
CC induce the proliferation of neural cells and regeneration of nerve and
CC brain tissue, and are useful for the treatment of central and peripheral
CC nervous system diseases and neuropathies, such as Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and amyotrophic lateral
CC sclerosis. The sequences are involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
CC cell disorders and platelet disorders such as thrombocytopenia,
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC disease. The sequences of the invention are also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia

CC gravis, allergic conditions such as asthma, thrombolysis or thrombosis
CC and coagulation disorders. Sequences ASG66666-ABG66758 represent human
XX novel polypeptides of the invention
SQ Sequence 374 AA;
Query Match 100.0%; Score 1106; DB 5; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEACRRDGGQLVSISEDEQKLE 60
DB 24 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEACRRDGGQLVSISEDEQKLE 83
QY 61 KFIENLLPSDGDGFWIGLRRREKOSNSTACQDLYAWTDGSIQFRNMYVDEPSCGSEVCV 120
DB 84 KFIENLLPSDGDGFWIGLRRREKOSNSTACQDLYAWTDGSIQFRNMYVDEPSCGSEVCV 143
QY 121 VMYHQPAPAGIGGPFQWDDRCNMKNFICKYSDKPAVPSREAGETELTTPVLP 180
DB 144 VMYHQPAPAGIGGPFQWDDRCNMKNFICKYSDKPAVPSREAGETELTTPVLP 203
QY 181 BETQEDAKTKFKESREAAALNLAY 204
DB 204 BETQEDAKTKFKESREAAALNLAY 227
RESULT 5
ADA54522
ID ADA54522 standard; protein; 374 AA.
XX
AC ADA54522;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein, SEQ ID 2090.
XX
XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
XX EPI293569-A2.
XX
XX 19-MAR-2003.
XX
XX 21-MAR-2002; 2002EP-00006586.
XX
XX 14-SEP-2001; 2001JP-0028381.
XX
XX 24-JAN-2002; 2002US-0350435P.
XX
XX (HELI-) HELIX RES INST.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isorai T, Sugiyama T, Otsuka K, Nagai K, Irie R, Tamechika I;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Masuho Y;
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
XX WPI; 2003-395539/38.
XX
XX N-PSDB; ADA52883.
XX
XX New polynucleotides encoding full-length polypeptides, e.g. secretory
XX and/or membrane proteins, useful for developing medicines for diseases in
XX which the gene is involved, or as target molecules for gene therapy.
XX
XX Claim 14; SEQ ID NO 2090; 205pp; English.
XX
XX The present invention relates to novel human secretory or membrane
XX proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
XX ADA54071). The coding sequences are useful in the gene therapy of
XX diseases caused by abnormalities of the proteins, e.g. cancer,
XX inflammatory diseases, osteoporosis or neurological disease.

XX
SQ Sequence 374 AA;
Query Match 100.0%; Score 1106; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEACRRDGGQLVSISEDEQKLE 60
DB 24 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEACRRDGGQLVSISEDEQKLE 83
QY 61 KFIENLLPSDGDGFWIGLRRREKOSNSTACQDLYAWTDGSIQFRNMYVDEPSCGSEVCV 120
DB 84 KFIENLLPSDGDGFWIGLRRREKOSNSTACQDLYAWTDGSIQFRNMYVDEPSCGSEVCV 143
QY 121 VMYHQPAPAGIGGPFQWDDRCNMKNFICKYSDKPAVPSREAGETELTTPVLP 180
DB 144 VMYHQPAPAGIGGPFQWDDRCNMKNFICKYSDKPAVPSREAGETELTTPVLP 203
QY 181 BETQEDAKTKFKESREAAALNLAY 204
DB 204 BETQEDAKTKFKESREAAALNLAY 227
RESULT 6
AAM25796
ID AAM25796 standard; protein; 387 AA.
XX
AC AAM25796;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:1311.
XX
XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW anti-inflammatory; antirheumatic; antithratic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnary; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder.
XX
XX Homo sapiens.
XX
XX WO200153455-A2.
XX
XX 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US035017.
XX
XX 23-DEC-1999; 99US-00471275.
XX
XX 21-JAN-2000; 2000US-00488725.
XX
XX 25-APR-2000; 2000US-00552317.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457603/49.
XX
XX N-PSDB; AAH39737.
XX
XX Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX
XX Claim 20; Page 272; 1217pp; English.
XX
XX PS

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and cells
CC they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antihaemic; antiaggregant; haemostatic; vulnery;
CC antiulcer; osteopathic; dermatological; antiallergic; antiaesthetic;
CC antidabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunosimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders
XX Sequence 387 AA;
SQ

Query Match	100.0%	Score 1106;	DB 4;	Length 387;
Best local Similarity	100.0%;	Prod. No. 3.4e-104;		
Matches 204;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GRLLSGGPVCRGGTQRCYKVIYFHDTSRRLLNPFSEAKEACRRDGGQLVSIESEDEQKLE	60	
Db	37	GRLLSGGPVCRGGTQRCYKVIYFHDTSRRLLNPFSEAKEACRRDGGQLVSIESEDEQKLE	96	
Qy	61	KFIENLLPSDGDWFILGRLRREKQSNSTACODLYAWTDGSIQFQNNWTVDEPFGSGSEVCV	120	
Db	97	KFIENLLPSDGDWFILGRLRREKQSNSTACODLYAWTDGSIQFQNNWTVDEPFGSGSEVCV	156	
Qy	121	VWYHQPAPAGIGGPFYQWDDRCNKMKNFICKYSDKPAVPSPREAGEGETELTTPVLP	180	
Db	157	VWYHQPAPAGIGGPFYQWDDRCNKMKNFICKYSDKPAVPSPREAGEGETELTTPVLP	216	
Qy	181	EETQEDAKKTFKSSREAAALNLAY	204	
Db	217	EETQEDAKKTFKSSREAAALNLAY	240	

RESULT 7
ADA54574
ID ADA54574 standard; protein; 374 AA.
XX
XX ADA54574;
XX
XX 20-NOV-2003 (first entry)
DT
XX Human protein, SEQ ID 2142.
XX
XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW Inflammatory disease; osteoporosis; neurological disease.
XX
XX Homo sapiens.
OS
XX
XX EPI293569-A2.
PN
XX
XX 19-MAR-2003.
PD
XX
XX 21-MAR-2002; 2002EP-00006586.
PF
XX
XX 14-SEP-2001; 2001JP-00328381.
PR
XX 24-JAN-2002; 2002US-0350435P.
PR
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
PA

XX	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI	Yamamoto J, Isono Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX	WPI: 2003-3955339/38.
DR	N-PSDB; ADA52935.
DR	
XX	
PT	New polynucleotides encoding full-length polypeptides, e.g. secretory
PT	and/or membrane proteins, useful for developing medicines for diseases in
PT	PT which the gene is involved, or as target molecules for gene therapy.
XX	
XX	Claim 14; SEQ ID NO 2142; 205pp; English.
PS	
XX	
CC	The present invention relates to novel human secretory or membrane
CC	proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC	ADA54071). The coding sequences are useful in the gene therapy of
CC	diseases caused by abnormalities of the proteins, e.g. cancer,
CC	inflammatory diseases, osteoporosis or neurological disease.
XX	
XX	Sequence 374 AA;
SQ	

Query Match	99.6%	Score 1102;	DB 6;	Length 374;
Best Local Similarity	99.5%;	Pred. No. 8.3e-104;		
Matches 203;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0
Qy	1	GRLLSGQPVCGGTORPCYKVIYFHDTSRRLNFEAAKACRRDGGQGVLSIESEDEQKLI	60	
Db	24	GRLLSGQPVCGGTORPCYKVIYFHDTSRRLNFEAAKACRRDGGQGVLSIESEDEQKLI	83	
Qy	61	KT ¹ ENLLPSDGFMTGLRRREEKQNSTACQDIYAWTDGSIQFRNMYVDEPSCGSEVCV	120	
Db	84	KT ¹ ENLLPSDGFMTGLRRREEKQNSTACQDIYAWTDGSIQFRNMYVDEPSCGSEVCV	143	
Qy	121	VMYHPSAPAGTGGPYMFQWNDRCNNKNFI ¹ CKYSDKPAVPSRAEGSETELTTTPVL	180	
Db	144	VMYHPSAPAGTGGPYMFQWNDRCNNKNFI ¹ CKYSDKPAVPSRAEGSETELTTTPVL	203	
Qy	181	ETQBEDAKTKFKSREAA ¹ NLAY	204	
Db	204	ETQBEDTKTKFKSREAA ¹ NLAY	227	

RESULT 8	
AAAY91490	
ID	AAAY91490 standard; protein; 374 AA.
XX	
XX	
XX	AAAY91490;
XX	
DT	29-JUN-2000 (first entry)
XX	
DE	Human secreted protein sequence encoded by gene 40 SEQ ID NO:163.
XX	
KW	Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW	antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
KW	osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
KW	antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
KW	immune disease; inflammation; blood disorder; tumour.
XX	
OS	Homo sapiens.
XX	
FN	WO200006698-A1.
XX	
PD	10-FEB-2000.
XX	
PF	29-JUL-1999; 99WO-US017130.
XX	
PR	30-JUL-1998; 98US-0094657P.
PR	05-AUG-1998; 98US-0095486P.
PR	06-AUG-1998; 98US-0095454P.
PR	06-AUG-1998; 98US-0095455P.
PR	12-AUG-1998; 98US-0096319P.
XX	

PA (HUNA-) HUMAN GENOME SCI INC.
 XX Komatsoulis GA, Rosen KA, Ruben SM, Duan R, Moore PA, Shi Y;
 PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
 PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
 XX WPI; 2000-195282/17.
 DR N-PSDB; AAA26385.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 PS Claim 11; Page 483-484; 634pp; English.
 XX
 CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the
 CC human secreted proteins given in AAY91451 to AAY91691. The human secreted
 CC proteins can have activities based on the tissues and cells they are
 CC expressed in. Examples of the activities are: cytostatic;
 CC immunosuppressive; anti-HIV; anti-inflammatory; neurotrophic; neuroprotective;
 CC anti-allergic; osteoprotective; antiarthritic; antibacterial; antidiabetic;
 CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
 CC corresponding secreted proteins are useful for preventing, treating or
 CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
 CC pathological conditions can be diagnosed by determining the amount of the
 CC proteins in a sample or by determining the presence of mutations in the
 CC polynucleotides. Specific uses are described for each of the
 CC polynucleotides, based on which tissues they are most highly expressed
 CC in, and include developing products for the diagnosis or treatment of
 CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
 CC and foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,
 CC Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
 CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
 CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
 CC reproductive disorders, gastrointestinal disorders, respiratory disorders
 CC and metabolic disorders. The proteins or polynucleotides can also be used
 CC as food additives or preservatives. The proteins are also useful for
 CC identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 374 AA;
 Query Match 99.1%; Score 1096; DB 3; Length 374;
 Best Local Similarity 99.0%; Pred. No. 3.4e-103;
 Matches 202; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GRLLSGQVCRGGTQPCYKVIYFHDTSRLNPFEEAKCRDGGQVLSIESDEQKLE 60
 DB 24 GRLLSGQVCRGGTQPCYKVIYFHDTSRLNPFEEAKCRDGGQVLSIESDEQKLE 83
 QY 61 KFIEHLLPSDGDFFWGLRRRREKQNSGTACODLYAWTDGSIQPRNWNVYDEPSCGSEVCV 120
 DB 84 XFIEHLLPSDGDFFWGLRRRREKQNSGTACODLYAWTDGSIQPRNWNVYDEPSCGSEVCV 143
 QY 121 VNYHQPSAPAGIGGPFYQWDDRCNKNPFIKYSDEKAVPSREAGETELTTPVLP 180
 DB 144 VNYHQPSAPAGIGGPFYQWDDRCNKNPFIKYSDEKAVPSREAGETELTTPVLP 203-
 QY 181 EETOEDAKTKFESREANLAY 204
 DB 204 EETOEDAKTKFESREANLAY 227
 RESULT 9
 ID AAY13367
 XX AAY13367 standard; protein: 382 AA.
 AC AAY13367;
 XX
 XX 25-JUN-1999 (first entry)
 DT
 XX Amino acid sequence of protein PRO234.
 DE

XX
 KW Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; AIDS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
 KW wound healing; tissue repair.
 XX
 OS Homo sapiens.
 XX
 PN WO9914328-A2.
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98WO-US019330.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059123P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 18-SEP-1997; 97US-0062125P.
 PR 18-SEP-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 17-OCT-1997; 97US-0063486P.
 PR 21-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063122P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 24-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 28-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 31-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 21-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066468P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 XX WPI; 1999-229533/19.
 DR

DR	N-PSDB; AAX52238.
XX	
PT	New isolated human genes and polypeptides used in, e.g. treatment of
PT	gastrointestinal ulceration.
XX	
XX	Claim 12; Fig 50; 320pp; English.
PS	
CC	
XX	AAY13344-403 represent secreted and transmembrane human proteins. The
CC	cDNA sequences are obtained from CDNA libraries, prepared from fetal
CC	lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
CC	encoded polypeptides have specific uses based on their homology to known
CC	polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
CC	with the preservation and maintenance of gastrointestinal mucosa and the
CC	repair of acute and chronic mucosal lesions (e.g. enterocolitis,
CC	Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
CC	microvillus atrophy), skin diseases associated with abnormal keratinocyte
CC	differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
CC	cell carcinoma of the vulva and gliomas), potent effects on cell growth
CC	and development, diseases related to growth or survival of nerve cells
CC	including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
CC	cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal
CC	scarring. PRO364 can be used as a target for anti-tumor drugs. PRO533 may
CC	be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
CC	be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
CC	have therapeutic applications in wound healing and tissue repair; PRO317
CC	can be used for treating problems of the kidney, uterus, endometrium,
CC	blood vessels, or related tissue, e.g. in the heart of genital tract
XX	
XX	Sequence 382 AA;
XX	SO

Query Match	98.7%;	Score 1092;	DB 2;	Length 382;
Best Local Similarity	96.2%;	Pred. No. 9e-103;		
Matches 204;	Conservative	0;	Mismatches 0;	Indels 8; Gaps 1;
QY	1	GRLLS-----	-GQVCRGGTQTPCKVYVFHDT	SRLNFEAKACRRDGGQLVSTES 52
Db	24	GRLLSASDLDIRGGQ	PVCRGGTQTPCKVYVFHDT	SRLNFEAKACRRDGGQLVSTES 83
QY	53	EDEQXLIKFIENLL	PSDGFWIGLRREKQKSNSTAC	QDLYAWTDGSIQFRNMYVDEP 112
Db	84	EDEQXLIKFIENLL	PSDGFWIGLRREKQKSNSTAC	QDLYAWTDGSIQFRNMYVDEP 143
QY	113	SCGSVCCVMYHQSAP	AGIGGPFYMFQWNNDRCKMKN	FFICKYSDEKPAVPSREAGESET 172
Db	144	SCGSVCCVMYHQSAP	AGIGGPFYMFQWNNDRCKMKN	FFICKYSDEKPAVPSREAGESET 203
QY	173	ELTTPLPEETOEDAK	KTFFESREAAINLAY	204
Db	204	ELTTPLPEETOEDAK	KTFFESREAAINLAY	235

RESULT 10	
ADC78457	
ID	ADC78457 standard; protein; 382 AA.
XX	
AC	ADC78457;
XX	
DT	01-JAN-2004 (first entry)
XX	
DE	Human PRO2334 protein.
XX	
KW	antiinflammatory; antitumor; cyrostatic; anipsoriatic; antiparkinsonian;
KW	neutrophic; neuroprotective; vasotropic; chemotactic; angiogenic;
KW	neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
KW	antiartherosclerotic; cardiant; antidiabetic; cerebroprotective;
KW	thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
KW	gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
KW	Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
KW	nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
KW	asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
KW	atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW	diabetes; stroke; gene therapy; transgenic; PRO; human.
XX	
XX	

OS	Homo sapiens.
XX	
XX	WO200015796-A2.
XX	
XX	23-MAR-2000.
XX	
XX	15-SEP-1999; 99WO-US021090.
XX	
XX	16-SEP-1998; 98WO-US019330.
XX	
XX	(GETH) GENENTECH INC.
XX	
XX	Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
PI	Yuan J;
PI	
XX	
DR	WPI: 2000-271434/23.
DR	N-FSDS; ADC78456.
XX	
XX	Novel nucleic acids encoding secreted and transmembrane polypeptides with
PT	homology, e.g. to growth and cancer-associated antigens.
XX	
XX	Claim 12; SEQ ID NO 137; 355bp; English.
PS	
XX	
CC	The invention relates to a novel nucleic acid encoding a PRO polypeptide.
CC	The polypeptides and polynucleotides of the invention may be useful as
CC	research tools and as therapeutics for treating enterocolitis, Zollinger-
CC	Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
CC	Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
CC	scarring and wound healing, nerve repair, rheumatoid arthritis, multiple
CC	cartilage formation, angiogenesis, asthma, thrombosis, bone and/or
CC	sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
CC	infertility, premature aging, AIDS, diabetes complications and stroke.
CC	The molecules may also be utilised during gene therapy procedures and
CC	transgenic animal production. The current sequence is that of the human
CC	PRO protein of the invention.
XX	
XX	Sequence 382 AA;
SQ	

Query Match	98.7%; Score 1092; DB 3; Length 382;
Best Local Similarity	96.2%; Pred. No. 9e-103;
Matches 204; Conservative	0; Mismatches 0; Indels 8; Gaps 1;
Qy 1	GRLLS-----GQPVCRGGTORPCVKVIYFHDTSRRLNFEFEAKACRDGGQLVSI
Db 24	GRLLSADLLRGQGPVCRGGTORPCVKVIYFHDTSRRLNFEFEAKACRDGGQLVSI
Qy 53	EDEQKUIEKPIENLLPSDGDGFWTGLRRREBKQNSACQDLYAWTDGSIQFRNYYVDEP
Db 84	EDEQKUIEKPIENLLPSDGDGFWTGLRRREBKQNSACQDLYAWTDGSIQFRNYYVDEP
Qy 113	SCSGEVCVVMYHQPAPAGIGGYPMQWDDRCNMKNFNICKYSDEKPAVPSREAGEET
Db 144	SCSGEVCVVMYHQPAPAGIGGYPMQWDDRCNMKNFNICKYSDEKPAVPSREAGEET
Qy 173	ELTTPVLPETQBEDAKTTFKESREAAALNLAY 204
Db 204	ELTTPVLPETQBEDAKTTFKESREAAALNLAY 235

RESULT 11
AAB80235
ID AAB80235 standard; protein; 382 AA.

DT 24-APR-2001 (first entry)

Human PRO234 protein.

xx
Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnery; cardiant;
KW antiangogenic; vasoprotic; antiaesthatic; antirheumatic; cancer;
KW antithrictic; antiinfertility; antidiabetic; antitumor; diabetes;
KW

KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 XX ischaemia; inflammation.
 OS Homo sapiens.
 XX WO200104311-A1.
 XX PD 18-JAN-2001.
 XX PF 22-FEB-2000; 2000WO-US004414.
 XX PR 07-JUL-1999; 99US-0143048P.
 XX PR 26-JUL-1999; 99US-0145698P.
 XX PR 28-JUL-1999; 99US-0146222P.
 XX PR 08-SEP-1999; 99WO-US020594.
 XX PR 13-SEP-1999; 99WO-US020344.
 XX PR 15-SEP-1999; 99WO-US021090.
 XX PR 15-SEP-1999; 99WO-US021547.
 XX PR 05-OCT-1999; 99WO-US023089.
 XX PR 30-NOV-1999; 99WO-US028214.
 XX PR 29-NOV-1999; 99WO-US028313.
 XX PR 02-DEC-1999; 99WO-US028564.
 XX PR 02-DEC-1999; 99WO-US028565.
 XX PR 16-DEC-1999; 99WO-US030095.
 XX PR 20-DEC-1999; 99WO-US030911.
 XX PR 20-DEC-1999; 99WO-US030999.
 XX PR 05-JAN-2000; 2000WO-US000219.
 XX (GETH) GENENTECH INC.
 XX PA Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 XX PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 XX PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
 XX PI Mather JP, Pan J, Paoni NF, Roy WA, Stewart TA, Tumas D;
 XX PI Williams EM, Wood WI;
 XX WPI; 2001-081051/09.
 XX N-PSDB; AAF72396.
 XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
 XX treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
 XX cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 XX disease).
 XX Claim 1; Fig 50; 393pp; English.
 XX The present sequence is one of sixty one novel secreted and transmembrane
 XX PRO polypeptides. The PRO polypeptides are useful for treating skin
 XX diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 XX gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 XX diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 XX cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
 XX ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
 XX disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
 XX infertility, AIDS and diabetes and retinal disorders such as retinitis
 XX pigmentosa. The PRO nucleic acids have applications in molecular
 XX biology, including use as hybridization probes, and in chromosome and
 XX gene mapping
 XX SQ Sequence 382 AA;
 Query Match 98.7%; Score 1092; DB 4; Length 382;
 Best Local Similarity 96.2%; Pred. No. 9e-103;
 Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
 QY 1 GRLS-----GQVCRGQTQPCVKYVYFHTSRLNFEAKEACRRDGGQLSVIES 52
 DB 24 GRLSASLDLREGQPCVCRGQTQPCVKYVYFHTSRLNFEAKEACRRDGGQLSVIES 83
 QY 53 EDEQKLEKFIENLLPSDGFWDWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEP 112
 DB 84 EDEQKLEKFIENLLPSDGFWDWGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYDEP 143

QY 113 SCGSEVCVMYHQPSAPAGIGGPPYMFQWMDRCNNKNNFKICKYDEKPAVPSREAGEET 172
 DB 144 SCGSEVCVMYHQPSAPAGIGGPPYMFQWMDRCNNKNNFKICKYDEKPAVPSREAGEET 203
 QY 173 ELTTVLPEETQEDAKKTFKESREAAALNLAY 204
 DB 204 ELTTVLPEETQEDAKKTFKESREAAALNLAY 235
 RESULT 12
 AAU29033
 ID AAU29033 standard; protein; 382 AA.
 XX AC AAU29033;
 XX DT 18-DEC-2001 (first entry)
 XX DE Human PRO polypeptide sequence #10.
 XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 XX KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 XX KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 XX KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200168848-A2.
 XX PD 20-SEP-2001.
 XX PF 28-FEB-2001; 2001WO-US006520.
 XX PR 01-MAR-2000; 2000WO-US005601.
 XX PR 02-MAR-2000; 2000WO-US005841.
 XX PR 03-MAR-2000; 2000US-0187202P.
 XX PR 06-MAR-2000; 2000US-0186968P.
 XX PR 14-MAR-2000; 2000US-0189320P.
 XX PR 14-MAR-2000; 2000US-0189328P.
 XX PR 15-MAR-2000; 2000WO-US006884.
 XX PR 21-MAR-2000; 2000US-0190828P.
 XX PR 21-MAR-2000; 2000US-0191007P.
 XX PR 21-MAR-2000; 2000US-0191048P.
 XX PR 21-MAR-2000; 2000US-0191314P.
 XX PR 28-MAR-2000; 2000US-0192655P.
 XX PR 29-MAR-2000; 2000US-0193032P.
 XX PR 29-MAR-2000; 2000US-0193053P.
 XX PR 30-MAR-2000; 2000WO-US008439.
 XX PR 04-APR-2000; 2000US-0194449P.
 XX PR 04-APR-2000; 2000US-0194647P.
 XX PR 11-APR-2000; 2000US-0195975P.
 XX PR 11-APR-2000; 2000US-0196000P.
 XX PR 11-APR-2000; 2000US-0196187P.
 XX PR 11-APR-2000; 2000US-0196690P.
 XX PR 11-APR-2000; 2000US-0196820P.
 XX PR 18-APR-2000; 2000US-0198121P.
 XX PR 18-APR-2000; 2000US-0198585P.
 XX PR 25-APR-2000; 2000US-0199397P.
 XX PR 25-APR-2000; 2000US-0199550P.
 XX PR 25-APR-2000; 2000US-0199654P.
 XX PR 03-MAY-2000; 2000US-0201516P.
 XX PR 17-MAY-2000; 2000WO-US013705.
 XX PR 22-MAY-2000; 2000WO-US014042.
 XX PR 30-MAY-2000; 2000WO-US014941.
 XX PR 02-JUN-2000; 2000WO-US015264.
 XX PR 05-JUN-2000; 2000US-0209832P.
 XX PR 28-JUL-2000; 2000WO-US020710.
 XX PR 22-AUG-2000; 2000US-00644848.
 XX PR 24-AUG-2000; 2000WO-US023328.
 XX PR 08-NOV-2000; 2000WO-US030952.
 XX PR 01-DEC-2000; 2000WO-US032678.
 XX PR 20-DEC-2000; 2000WO-US034956.
 XX (GETH) GENENTECH INC. PA

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XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-602746/68.
DR N-PSDB; AAS45934.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX Claim 11; Fig 20; 774pp; English.
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX SQ Sequence 382 AA;
Query Match 98.7%; Score 1092; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
Qy 1 GRLLS-----CQPVCRGQTQPCYKVIYFHDTSRLNFEEAKACRRDGGQLVSIES 52
Db 24 GRLLSASDLRLGQPVCRGQTQPCYKVIYFHDTSRLNFEEAKACRRDGGQLVSIES 83
Qy 53 EDEQKLIETIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEP 112
Db 84 EDEQKLIETIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEP 143
Qy 113 SCGSEVCVMVHQPAPAGIGPWFQNDRCNMKNFCKYSDEKPAVPSREAGEET 172
Db 144 SCGSEVCVMVHQPAPAGIGPWFQNDRCNMKNFCKYSDEKPAVPSREAGEET 203
Qy 173 ELTPVLPEETQEDAKKTKPESREAAALNLAY 204
Db 204 ELTPVLPEETQEDAKKTKPESREAAALNLAY 235
RESULT 13
ABUS8409
ID ABUS8409 standard; protein; 382 AA.
XX AC ABUS8409;
XX DT 15-APR-2003 (first entry)
XX DE Human PRO polypeptide #10.
XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
XX KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX
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PF 21-JUN-2002; 2002US-00176492.
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 28-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
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PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
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PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078865P.
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PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
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PR	10-JUN-1998;	98US-0088722P.	PR	10-SEP-1998;	98US-0099812P.
PR	10-JUN-1998;	98US-0088738P.	PR	15-SEP-1998;	98US-0100388P.
PR	10-JUN-1998;	98US-0088740P.	PR	16-SEP-1998;	98US-0100662P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100664P.
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PR	22-JUN-1998;	98US-0090252P.	PR	24-SEP-1998;	98US-0101922P.
PR	22-JUN-1998;	98US-0090254P.	PR	25-SEP-1998;	98US-0101786P.
PR	24-JUN-1998;	98US-0090429P.	PR	29-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090435P.	PR	29-SEP-1998;	98US-0102240P.
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PR	02-SEP-1998;	98US-0098843P.			
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PR	10-SEP-1998;	98US-0099754P.			

Query Match 98.7%; Score 1092; DB 6; Length 382;
 Best Local Similarity 96.2%; Pred. No. 9e-103;
 Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY	1	CELLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGOLVSIES 52
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QY	53	EDEQKLEKFIENLLPSDGFWIGLRREEKQSNSTACQDLYAMTDGSIQFRNYYVDEP 112
DB	84	EDEQKLEKFIENLLPSDGFWIGLRREEKQSNSTACQDLYAMTDGSIQFRNYYVDEP 143
QY	113	SCGSEVCVYVNHQSPAPAGIGGPFYQWDDRCNKNFNICKYSDKPAVPSRAEGEET 172
DB	144	SCGSEVCVYVNHQSPAPAGIGGPFYQWDDRCNKNFNICKYSDKPAVPSRAEGEET 203
QY	173	ELTTPVLPETQEDAKKTFKESREALNLAY 204
DB	204	ELTTPVLPETQEDAKKTFKESREALNLAY 235

RESULT 14
 ABU71613
 ID ABU71613 standard; protein; 382 AA.
 XX AC ABU71613;
 XX DT 16-JUN-2003 (first entry)
 XX DE Human PRO polypeptide #24.
 XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW pathological disorder; cardiac insufficiency disorder; protein secretion;
 KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
 KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
 KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;

KW cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal;
KW antiulcer; dermatological; vulnery.
XX
OS Homo sapiens.
XX
XX US2002146709-A1.
XX
XX 10-OCT-2002.
XX
XX 18-JUN-2001; 2001US-00909088.
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XX 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
XX 17-SEP-1997; 97US-0059117P.
XX 17-SEP-1997; 97US-0059119P.
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XX 17-SEP-1997; 97US-0059184P.
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XX 03-NOV-1997; 97US-0064248P.
XX 07-NOV-1997; 97US-0064809P.
XX 12-NOV-1997; 97US-0065186P.
XX 17-NOV-1997; 97US-0065846P.
XX 18-NOV-1997; 97US-0065693P.
XX 21-NOV-1997; 97US-0066120P.
XX 21-NOV-1997; 97US-0066364P.
XX 24-NOV-1997; 97US-0066453P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066511P.
XX 24-NOV-1997; 97US-0066770P.
XX 24-NOV-1997; 97US-0066772P.
XX 24-NOV-1997; 97US-0066772P.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 01-DEC-1998; 98WO-US025108.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US030999.
PR 11-FEB-2000; 2000WO-US00219.
PR 22-FEB-2000; 2000WO-US003565.
PR 24-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005004.
PR 20-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US007377.
PR 22-MAY-2000; 2000WO-US008439.
PR 02-JUN-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US015264.
PR 24-AUG-2000; 2000WO-US020710.
PR 18-SEP-2000; 2000WO-US023328.
XX 2000US-00655350.
PA (GETH) GENENTECH INC.
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavlin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-328338/31.
DR N-PSDB; ACA59008.
XX Isolated nucleic acid useful for e.g., treating pathological disorders
XX encodes a secreted or transmembrane protein.
XX Claim 12; Fig 50; 473pp; English.
XX The invention relates to human PRO polypeptides (secreted or
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX PRO polypeptides and polynucleotides can be used in treating pathological
XX disorders and tumors, in therapeutic treatment of cardiac insufficiency
XX disorders and in therapeutic treatment of disorders involving protein
XX secretion by the pancreas, including diabetes. They can also be used in
XX treating disorders associated with the preservation and maintenance of
XX gastrointestinal mucosa and the repair of acute and chronic mucosal
XX lesions, and skin diseases associated with abnormal keratinocyte
XX differentiation (e.g., psoriasis, epithelial cancers such as lung
XX squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
XX The sequences can be used as molecular markers for protein
XX electrophoresis purposes and can be utilised in protein-protein binding
XX assays, biochemical screening assays, immunoassays and cell-based assays.
XX This sequence represents a human PRO polypeptide of the invention
XX
XX
SQ Sequence 382 AA;

Query Match 98.7%; Score 1092; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 GRLLS-----GQVCEGGTQPCYKVIYFHDTSRLNFEAEACRRDGGQLVSIES 52
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QY 53 EDEQKLIKFIENLLPSDGFWMGLRRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEP 112
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QY 173 ELTTPVLPETQEDAKTFKESREAAALNLAY 204
DB 204 ELTTPVLPETQEDAKTFKESREAAALNLAY 235

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ABU87957
ID ABU87957 standard; protein; 382 AA.
XX AC ABU87957;
XX DT 07-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO234.
XX KW Human; secreted and transmembrane protein: PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
XX PN US2003032127-A1.
XX PD 13-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183012.
XX PR 18-SEP-1997; 97US-0059263P.
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PR 21-OCT-1997; 97US-0063486P.
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PR 06-MAY-1998; 98US-0084414P.
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Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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DB 84 EDEQKLEKIEIENLLPSDGFNGLRRREKQSNSTACQDLAWTQDGSIQFRNWTVD 143
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RESULT 16
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XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
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XX PD 13-FEB-2003.
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Pred. No. 9e-103;

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XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
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XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003027278-A1.
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XX 06-FEB-2003.
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XX PD 13-FEB-2003.
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Query Match 98.7%; Score 1092; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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RESULT 21
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XX AC ABUS9836;
XX DT 11-AUG-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO234.
XX KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
XX KW chondrocyte differentiation; tumour necrosis factor-alpha release;
XX KW affinity purification.
XX OS Homo sapiens.
XX PN US2003036147-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00187741.
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Query Match 98.7%; Score 1092; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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DT 10-JUN-2003 (first entry)
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KW Alzheimer's disease; ischaemia; cytostatic; neurotropic; vasotropic;
KW neuroprotective.
XX
OS Homo sapiens.
XX
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XX
PD 19-DEC-2002.
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PF 10-JUL-2001; 2001US-00902853.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
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PR 05-JAN-2000; 2000WO-US000219.
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PR 24-FEB-2000; 2000WO-US004414.
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PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams FM, Wood WI;
XX WPI; 2003-361832/34.

DR N-PSDB; ACA58405.
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX Claim 12; Fig 50; 474pp; English.
XX The present invention relates to the isolation of novel human secreted
CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
CC sequences encoding them. The polynucleotide sequences are useful in
CC molecular biology, as hybridisation probes, in chromosome and gene
CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide sequences may also be used in preparing PRO polypeptides
CC by recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptides or
CC their antibodies are useful in preparing a medicament for treating a
CC condition responsive to the polypeptide or antibody, such as cancer,
CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
CC ABU71445-ABU71505 represent human PRO polypeptides of the invention
XX Sequence 382 AA;
SQ
Query Match 98.7%; Score 1092; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
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DB 24 GRLLSASDLDRGGQVCRGGTQRCYKVIYPHDTSRLNFEAKACRRDGGQLVSTES 83
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DB 84 EDEQKLEKFIENLLPSDGDGFWIGLRREKQSGNSTACQDLYAWTDGSIQFRNHYVDEP 143
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AC ABR68085;
XX 11-AUG-2003 (first entry)
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XX Human; PRO; secreted protein; transmembrane protein; TNF-alpha;
KW extracellular domain; tumour necrosis factor-alpha; cartilage disorder;
KW chondrocyte proliferation; differentiation; cancer; tumour; diagnosis;
KW bone disorder; arthritis; sports injury; cancer; kidney; cervix;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX Homo sapiens.
OS
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XX US2003027264-A1.
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XX PD 06-FEB-2003.
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Best Local Similarity 96.2%; Pred. No. 9e-103;
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RESULT 24
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ID ABU96138 standard; protein; 382 AA.
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AC ABU96138;
XX
DT 25-JUL-2003 (first entry)
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DE Novel human secreted and transmembrane protein PRO234.
XX
KW Human; secreted and transmembrane protein; PRO; transgenic animal;
KW knockout; chromosome identification; tissue typing; tumour;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumor necrosis factor-alpha release stimulator.
XX
OS Homo sapiens.
XX
FN US2003036144-A1.
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PD 20-FEB-2003.
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PF 01-JUL-2002; 2002US-00187601.
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KW	tumour necrosis factor-alpha; gene therapy.
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GenCore version 5.1.6
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Listing first 45 summaries

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SUMMARIES

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6	561.5	50.8	273	4	US-09-638-203-2
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9	231	20.9	115	4	US-09-489-847-324
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ALIGNMENTS

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; Patent No. 6476195
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; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
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US-09-489-847-166

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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Goddard, A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-137

Query Match 98.7%; Score 1092; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 5.5e-106;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GLLIS-----GQVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQLVGIES 52
DB 24 GLLSASDLDRGGQVCRGGTQPCYKVIYFHDTSRLNFEFEAKACRRDGGQLVGIES 83
QY 53 EDEQKLEKFIENLLPSDGFWMGLRREKQSNSTACQDLYAWMTDGSISQFRNYYVDEP 112
DB 84 EDEQKLEKFIENLLPSDGFWMGLRREKQSNSTACQDLYAWMTDGSISQFRNYYVDEP 143
QY 113 SCGSEVCVMYHQPAPAGIGGYPYFQWDDRCNNKNNFICKYSDEKPAVPSREAEGET 172
DB 144 SCGSEVCVMYHQPAPAGIGGYPYFQWDDRCNNKNNFICKYSDEKPAVPSREAEGET 203
QY 173 ELTTPVLPETQEDAKTKFKESREAAALNLAY 204
DB 204 ELTTPVLPETQEDAKTKFKESREAAALNLAY 235

RESULT 3
US-09-905-125A-137
; Sequence 137, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-137

Query Match 98.7%; Score 1092; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 5.5e-106;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

Qy 1 GRLLS-----GQVCRGGTQPCYKVIYFHTDSRLNFEAKEACRRDGGQVLSIES 52
Db 24 GRLLSASDLDRGGQPCVCRGGTQPCYKVIYFHTDSRLNFEAKEACRRDGGQVLSIES 83
Qy 53 EDEQKLEKFIENLLPSDGDGFWIGLRREKQKSNSTACQDLYAWTDGSIQFRNYYVDEP 112
Db 84 EDEQKLEKFIENLLPSDGDGFWIGLRREKQKSNSTACQDLYAWTDGSIQFRNYYVDEP 143
Qy 113 SCGSEVCVMYHQPAPAGIGGPTMFWQNDRCNMKNFKICKYSDKXPVPSREAGEET 172
Db 144 SCGSEVCVMYHQPAPAGIGGPTMFWQNDRCNMKNFKICKYSDKXPVPSREAGEET 203
Qy 173 ELTTPVLPEETOEDAKKTFKESREAAINLAY 204
Db 204 ELTTPVLPEETOEDAKKTFKESREAAINLAY 235

RESULT 4
US-09-902-775A-137
; Sequence 137, Application US/09902775A
; Patent No. 6886451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10456-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-137

Query Match 98.7%; Score 1092; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 5.5e-106;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

Qy 1 GRLLS-----GQVCRGGTQPCYKVIYFHTDSRLNFEAKEACRRDGGQVLSIES 52
Db 24 GRLLSASDLDRGGQPCVCRGGTQPCYKVIYFHTDSRLNFEAKEACRRDGGQVLSIES 83
Qy 53 EDEQKLEKFIENLLPSDGDGFWIGLRREKQKSNSTACQDLYAWTDGSIQFRNYYVDEP 112
Db 84 EDEQKLEKFIENLLPSDGDGFWIGLRREKQKSNSTACQDLYAWTDGSIQFRNYYVDEP 143
Qy 113 SCGSEVCVMYHQPAPAGIGGPTMFWQNDRCNMKNFKICKYSDKXPVPSREAGEET 172

EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 234
LENGTH: 82
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (82)
OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-234

Query Match 20.9%; Score 231; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 8.4e-17; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRR 42
Db 24 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRR 65

RESULT 9

US-09-489-847-324
Sequence 324, Application US/09489847
Patent No. 6476195

GENERAL INFORMATION:

APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031P1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 324
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens

US-09-489-847-324

Query Match 20.9%; Score 231; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e-16; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRR 42
Db 58 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAKEACRR 99

RESULT 10

US-09-976-594-168
Sequence 168, Application US/09976594
Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 168
LENGTH: 1456
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: incyte ID No. 6673549 1674368CD1
US-09-976-594-168

Query Match 16.5%; Score 182; DB 4; Length 1456;

Best Local Similarity 25.5%; Pred. No. 5.6e-10; Indels 54; Gaps 8;
Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;

Qy 19 YKVIYFHDTSRLNFEAKEACRRDGGQLVSTESDEQKLEKFIENLLPSDGFWIGLR 78
Db 807 YKDYQYFSEKKEITMDNARAFCKRNFGLVSIQSEKFLWKYV-NRNDASAYFIGLL 865

Qy 79 RREKOSNSTACQDLYAWTDGSIQSRNRYVDEPSCGS--EVCVVVYHQPSPAPAGIGGPY 136
Db 866 ISLDKK-----FAWMDGSKVDYVSWATGEPFANEDENCVTMY-----SNSGF---- 908

Qy 137 MFQWDDRCNMKNFTICKYSDEK----PAVPSREAGEDETELTTPVLPPEOTB----- 185
Db 909 ---WNDINGYPNFTICQSHSSINATTWP-----TSPSVPSGCKEKGWNFYSN 954

Qy 186 -----EDAKTFFKESERAA 200

Db 955 KCFKIFGFMEERKQWQEARACI 978

RESULT 11

US-08-840-062-5
Sequence 5, Application US/08840062
Patent No. 6117977

GENERAL INFORMATION:

APPLICANT: LASKY, LAURENCE A.
APPLICANT: WU, KAI
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,062
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1019R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881

```

; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-840-062-5

Query Match 16.1%; Score 178.5; DB 3; Length 1455;
Best Local Similarity 25.9%; Pred. No. 1.3e-09;
Matches 53; Conservative 33; Mismatches 56; Indels 53; Gaps 8;

QY 19 YKVIYFHTSRLNFEAKACRRDGGQGLVSISEDEQKLIKFIENLPSDGDGFWIGLR 78
Db 806 YKDQYYSKEKETMDNARFCKNFGDLATIKSEKFLWKYI-NKNGGQSPYPIGML 864
QY 79 RREKQSNSTACQDIYAWTSGISQFRNYYVDEPSCGS--FVGVVYHQPSAPAGIGPY 136
Db 865 ISMDKK-----FIMDGSKYDFVAWATGEPNFANDDENCVTMY-----TNSGF----- 907
QY 137 MFQWDDRCNMKNPFICK---YSDEKPAVPSREAEGEBETELTTPVLPEETQE----- 185
Db 908 ---WNDINCYPNFIQHNSSINATAMP-----TTPTFGCKEGHLYKNK 953
QY 186 -----EDAKTFKSSREALNL 202
Db 954 CFKIFGFANEKSKWQDARQACKGL 978

RESULT 12
US-08-840-062-4
; Sequence 4, Application US/08840062
; Patent No. 6117977
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: WU, KAI
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,062
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1019R1
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1479 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-840-062-4

Query Match 16.0%; Score 176.5; DB 3; Length 1479;
Best Local Similarity 30.4%; Pred. No. 2.1e-09;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;

QY 15 QRPCVKVIYFHTSRLNFEAKACRRDGGQGLVSISEDEQKLIKFIENLPSDGDGFW 74
Db 1037 QGHCHYR--YF---AHRRAWEDAECDRRRAGHLTSHVSPHEHKFINSF-----CHENSW 1085
QY 75 IGLRREKQSNSTACQDIYAWTSGISQFRNYYVDEPS---CGSEVCVVMYHQPSAPAG 131
Db 1086 IGLNDRTVRDE-----FQWTDNTGLQYENWREKQPDNPFAGGDCVVMVAHENG--- 1134
QY 132 IGGPYMFQWDDRCNMKNPFICK 154

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; TOPOLOGY: Linear
US-08-840-062-2

Query Match      15.4%; Score 170.5; DB 3; Length 1479;
Best Local Similarity 31.4%; Pred.No.9.1e-09;
Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;

QY      5  SQPCVCRGGTQREPCYKVIYFHDTSRLNPEEAKACRRDGGQGVLSIESDEQKLIKIEFKIE 64
DB      384  SNQPF-----QHCYRL-----QAERKSQWESKRACLRGGDLLSIHSMALEFIFTKQIK 433

QY      65  NLLPSDGDWFWIGLRREEKQSNSTACQDLYANTDGSISQFRNMYVDEPS---CGSEVCVV 121
DB      434  QEVE---ELWIGL-----NDLKLQMNFEWSGDGLSVFTTHHPPEPNFRDLSLEDCVT 482

QY      122  MYHQPSAPAGIGGYPWFQWMDRCKMKNNFICK 154
DB      483  IW-----GPEG-----RWNDSFCNQSLFSICK 504

RESULT 16
PCT-US95-03747-2
; Sequence 2. Application PC/TUS9503747
; GENERAL INFORMATION:
; APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
; TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03747
; FILING DATE: 27-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Imbra, Richard J.
; REGISTRATION NUMBER: 37,643
; REFERENCE/DOCKET NUMBER: FP-LJ 1453
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-03747-2

Query Match      13.7%; Score 152; DB 5; Length 912;
Best Local Similarity 28.8%; Pred.No.4.1e-07;
Matches 47; Conservative 17; Mismatches 61; Indels 38; Gaps 8;

QY      15  QRPCYKVIYFHDTSRLNPEEAKACRRDGGQGVLSIESDEQKLIKIEFKIEFENLLPSDGDWF 74
DB      697  QGACYK----HFSARR-SWEEAKENKCMYGAHLASISTPEEQDFINNRYEQ-----W 745

QY      75  IGLRREEKQSNSTACQDLYANTDGSISQFRNMYVDEPS---CGSEVCVVW-YHQPSAPA 130
DB      746  IGL-----NDRITIEGFLWSDGVGPALLYENWNPQGPSYFLSGENCVVMVWHDQG--- 794

QY      131  GIGGYPWFQWMDRCKMKNNFICKYS----DEKPAVPSREAEG 169
DB      795  -----QWSDVPCNHYLSITCKMGLVSCGPPPEPLAEVFG 829

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RESULT 17
US-09-602-877A-99
; Sequence 99, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu Jianshun C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-602-877A-99

Query Match      13.7%; Score 151; DB 4; Length 197;
Best Local Similarity 25.0%; Pred. No. 6.5e-08;
Matches 38; Conservative 26; Mismatches 64; Indels 24; Gaps 4;

QY      7 QPCVCGGTQ--RPCVKVIYPHDTSRRLNFEAKACRRDGGQLVSISEDEQKLIKIEFIE 64
DB      65 QTVCLRGTKVHKCYLA-----SEGLKHFHEANEDCISKGLIVIPNSDEINALQDYGK 119

QY      65 NLPDSDGDFWIGLRRREKQSNSTACQDLYAWTDGSIQFNNYVDPEPSCGSEVVMYH 124
DB      120 RSLPGVNDFMLGI-----NDMVTEGKFVDVNGIAISFLNWDRAQPNCGKRENCVLFS 171

QY      125 QPSAPAGIGGPPYFQWDDRCNMKNFICKYS 156
DB      172 QSA-----QKWSDEACRSKRICEFT 194

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RESULT 18
US-09-866-028-50
; Sequence 50, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 50
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-50

```

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Query Match      13.5%; Score 149.5; DB 4; Length 455;
Best Local Similarity 25.6%; Pred. No. 2.9e-07;
Matches 45; Conservative 25; Mismatches 61; Indels 45; Gaps 8;

QY      12 GGTQPCYKVIY--PHDTSRLN-----FEEAKACRRDGGQLVSISEDEQK 57
DB      287 GGAQ--CATKVHPFHTCDLRIDGCFWVSSEADTYEARMKCQKGGVLAQIKSQYQD 344

QY      58 LIEKFIENLLP-----SDGD-----FWIGLRRREKQSNSTACQDLYAWTDGSIQFNNY 108
DB      345 ILAFYLGLLETTNEVTDSDFTNRNFWIGLTYKTAK-----DSFRWATGEHQAFISFA 396

QY      109 VDEPSCGSEVVMYHQPSAPAGIG-----GPMFQWDDRCNMKNFICKYSDE 158
DB      397 FQPDNHLGLVWL-----SAAAGFCNCVELQASAAFNWDDQCKTRNRYICQFAQE 446

RESULT 19
US-07-641-971B-1
; Sequence 1, Application US/07641971B
; Patent No. 5236706
; GENERAL INFORMATION:
; APPLICANT: Debre, Patrice
; APPLICANT: Mossalayi, Mohammed D
; TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE
; TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Irving M. Fishman, CIBA-GEIGY Corporation
; STREET: 556 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/641,971B
; FILING DATE: 19910116
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 90016254
; FILING DATE: 24-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fishman, Irving M
; REGISTRATION NUMBER: 30258
; REFERENCE/DOCKET NUMBER: 4-17921/*-DEB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-277-4832
; TELEFAX: 908-277-4306
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; CELL TYPE: Human B. Cells
; CELL LINE: CHO cells transformed with pCAL8-BF-ND
US-07-641-971B-1

Query Match      13.5%; Score 149; DB 1; Length 174;
Best Local Similarity 30.2%; Pred. No. 8.9e-08;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY      15 QPCYKVIYPHDTSRRLNFEAKACRRDGGQLVSISEDEQKLIKIEFNLPSDGDWF 74

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Db 24 QKCY---YFGKTKQ--WVHARYACDDMEGQLVSIHSPEDFLTKH-----ASHTGSW 73

Qy 75 IGLRREKQSNSTACQDLYAWTDGSIQFRNRYVDEPSCGS--EVCVVMYHQPAPAGI 132

Db 74 IGLRNLDLKGE-----FIWVDGSHVDYSNAPGEPTRSOGEDCVMM-----RGS 118

Qy 133 GGPYMFQWDDRCNMK--NNFICKYSDEKPAV---PSREAEGE-----ETELTTPV 178

Db 119 G-----RWDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGDPDRPDGRLPTPS 169

Qy 179 LP 180

Db 170 AP 171

RESULT 20

US-07-781-248A-1

; Sequence 1, Application US/07781248A

; Patent No. 5246699

; GENERAL INFORMATION:

; APPLICANT: Debre, Patrice

; APPLICANT: Mossalavi, Mohammed D

; TITLE OF INVENTION: MATURATION OF HEMATOPOIETIC CELLS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation

; STREET: 556 Morris Avenue

; CITY: Summit

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07901

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0; Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/781,248A

; FILING DATE: 19911230

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 90103565

; FILING DATE: 09-MAY-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Ikeler, Barbara J.

; REGISTRATION NUMBER: 36,170

; REFERENCE/DOCKET NUMBER: 4-18065/A/DEB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-277-3368

; TELEFAX: 908-277-4306

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 174 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; CELL TYPE: Human B. Cells

; CELL LINE: CHO cells transformed with pCAL8-BF-ND

US-07-781-248A-1

Query Match 13.5%; Score 149; DB 1; Length 174;

Best Local Similarity 30.2%; Pred. No. 9.9e-08;

Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

Qy 15 QRPCKVVIYFHTGTRRLNFEAKACRRDGGQLVSIHSPEDFLTKH-----ASHTGSW 74

Db 24 QKCY---YFGKTKQ--WVHARYACDDMEGQLVSIHSPEDFLTKH-----ASHTGSW 73

Qy 75 IGLRREKQSNSTACQDLYAWTDGSIQFRNRYVDEPSCGS--EVCVVMYHQPAPAGI 132

Db 74 IGLRNLDLKGE-----FIWVDGSHVDYSNAPGEPTRSOGEDCVMM-----RGS 118

Qy 133 GGPYMFQWDDRCNMK--NNFICKYSDEKPAV---PSREAEGE-----ETELTTPV 178

Db 119 G-----RWDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGDPDRPDGRLPTPS 169

Qy 179 LP 180

Db 170 AP 171

RESULT 21

US-08-365-103B-10

; Sequence 10, Application US/08365103B

; Patent No. 5766943

; GENERAL INFORMATION:

; APPLICANT: Lynch, Richard G

; APPLICANT: Nurez, Raphael D.

; APPLICANT: Yocoi, Jungi

; TITLE OF INVENTION: DNA Sequences for Soluble Proms of CD23

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Zarley, McKee, Thomte, Voorhees & Sease

; STREET: 801 Grand Ave. Suite 3200

; CITY: Des Moines

; STATE: Iowa

; COUNTRY: United States

; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0; Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/365,103B

; FILING DATE: 28-DEC-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Nebel, Heidi S.

; REGISTRATION NUMBER: 37,719

; REFERENCE/DOCKET NUMBER: UIxf N5-24

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (515) 288-3667

; TELEFAX: (515) 288-1338

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 320 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-365-103B-10

Query Match 13.5%; Score 149; DB 1; Length 320;

Best Local Similarity 30.2%; Pred. No. 2e-07;

Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

Qy 15 QRPCKVVIYFHTGTRRLNFEAKACRRDGGQLVSIHSPEDFLTKH-----ASHTGSW 74

Db 170 QKCY---YFGKTKQ--WVHARYACDDMEGQLVSIHSPEDFLTKH-----ASHTGSW 219

Qy 75 IGLRREKQSNSTACQDLYAWTDGSIQFRNRYVDEPSCGS--EVCVVMYHQPAPAGI 132

Db 220 IGLRNLDLKGE-----FIWVDGSHVDYSNAPGEPTRSOGEDCVMM-----RGS 264

Qy 133 GGPYMFQWDDRCNMK--NNFICKYSDEKPAV---PSREAEGE-----ETELTTPV 178

Db 265 G-----RWDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGDPDRPDGRLPTPS 315

Qy 179 LP 180

US-09-517-605-2

Query Match 13.1%; Score 144.5; DB 4; Length 404;
Best Local Similarity 29.7%; Pred. No. 8.2e-07;
Matches 47; Conservative 23; Mismatches 47; Indels 41; Gaps 10;
QY 23 YFHTSRLNFEAKACRRDGGQLYSIESEDEQKLIETIENLLPSDGDVWIGLRRRE 82
Db 268 YFMSNSQR-NWHDSTITACKVGAQLVVIKSAEQNFLOLQSSR---SNRTWMLSLDLNQ 323
QY 83 KQSNSTACODLYAW--TDGSI--QFRNMYVDPS--CGSEVCVMYHOPSPAPAGIGGPPYM 137
Db 324 -----IGKMTWVGTNKTLTKEAENWGAGFPNNKSKEDCVEIYIKRERDSG----- 140
QY 138 FQWDDRCNMKNFICKYSDEKPAVPSREAEGET 172
Db 141 -KWDDACHKRAALCYTASQPGSCNGRGECEVET 174
QY 139 QWDDRCNMKNFICKYS-----DEK-----PAVPS 164
Db 364 -WDDKCNLAKFWICKKSAASCSRDEEQFLSPAPATFN 400.

RESULT 25

US-08-513-278-4
Sequence 4, Application US/08513278
Patent No. 5840844
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 565D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-513-278-4
Query Match 13.0%; Score 143.5; DB 2; Length 372;
Best Local Similarity 25.5%; Pred. No. 9.3e-07;
Matches 41; Conservative 37; Mismatches 50; Indels 27; Gaps 8;

QY 24 FHTSRLNFEAKACRRDGGQLYSIESEDEQKLIETIENLLP-SGDFTWIGLRRRE 82
Db 41 YHYSEKPMWENARKPKQNYTDLVAIQNKR---IE-YLENTLPKSPYYWIGIRK--- 93
QY 83 KQSNSTACODLYAW--TDGSI--QFRNMYVDPS--CGSEVCVMYHOPSPAPAGIGGPPYM 137
Db 94 -----IGKMTWVGTNKTLTKEAENWGAGFPNNKSKEDCVEIYIKRERDSG----- 140
QY 138 FQWDDRCNMKNFICKYSDEKPAVPSREAEGET 172
Db 141 -KWDDACHKRAALCYTASQPGSCNGRGECEVET 174

Search completed: September 9, 2004, 22:58:15
Job time : 17.0393 secs

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